#3

<110> U.S. Army Medical Research & Material Command

<120> RECOMBINANT VACCINE AGAINST BOTULINUM NEUROTOXIN

<130> A33626-A 067252.0107

<150> PCT/US00/12890
<151> 2000-05-12

<150> 09/611,419
<151> 2000-07-06

<150> 60/133,865
<151> 1999-05-12

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<151> 1993-09-21

<160> 34

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 1332
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct based on Clostridium botulinum sequence

<221> CDS
<222> (13)...(1326)

<400> 1
gaattcgaaa cg atg cgt ctg ctg tct acc ttc act gaa tac atc aag aac 51
Met Arg Leu Leu Ser Thr Phe Thr Glu Tyr Ile Lys Asn
1 5 10

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atc atc aat acc tcc atc ctg aac ctg cgc tac gaa tcc aat cac ctg   99
Ile Ile Asn Thr Ser Ile Leu Asn Leu Arg Tyr Glu Ser Asn His Leu
     15                  20                  25

atc gac ctg tct cgc tac gct tcc aaa atc aac atc ggt tct aaa gtt  147
Ile Asp Leu Ser Arg Tyr Ala Ser Lys Ile Asn Ile Gly Ser Lys Val
 30                  35                  40                  45

aac ttc gat ccg atc gac aag aat cag atc cag ctg ttc aat ctg gaa  195
Asn Phe Asp Pro Ile Asp Lys Asn Gln Ile Gln Leu Phe Asn Leu Glu
                 50                  55                  60

tct tcc aaa atc gaa gtt atc ctg aag aat gct atc gta tac aac tct  243
Ser Ser Lys Ile Glu Val Ile Leu Lys Asn Ala Ile Val Tyr Asn Ser
             65                  70                  75

atg tac gaa aac ttc tcc acc tcc ttc tgg atc cgt atc ccg aaa tac  291
Met Tyr Glu Asn Phe Ser Thr Ser Phe Trp Ile Arg Ile Pro Lys Tyr
         80                  85                  90

ttc aac tcc atc tct ctg aac aat gaa tac acc atc atc aac tgc atg  339
Phe Asn Ser Ile Ser Leu Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met
     95                 100                 105

gaa aac aat tct ggt tgg aaa gta tct ctg aac tac ggt gaa atc atc  387
Glu Asn Asn Ser Gly Trp Lys Val Ser Leu Asn Tyr Gly Glu Ile Ile
110                 115                 120                 125

tgg act ctg cag gac act cag gaa atc aaa cag cgt gtt gta ttc aaa  435
Trp Thr Leu Gln Asp Thr Gln Glu Ile Lys Gln Arg Val Val Phe Lys
                130                 135                 140

tac tct cag atg atc aac atc tct gac tac atc aat cgc tgg atc ttc  483
Tyr Ser Gln Met Ile Asn Ile Ser Asp Tyr Ile Asn Arg Trp Ile Phe
            145                 150                 155

gtt acc atc acc aac aat cgt ctg aat aac tcc aaa atc tac atc aac  531
Val Thr Ile Thr Asn Asn Arg Leu Asn Asn Ser Lys Ile Tyr Ile Asn
        160                 165                 170

ggc cgt ctg atc gac cag aaa ccg atc tcc aat ctg ggt aac atc cac  579
Gly Arg Leu Ile Asp Gln Lys Pro Ile Ser Asn Leu Gly Asn Ile His
    175                 180                 185

gct tct aat aac atc atg ttc aaa ctg gac ggt tgt cgt gac act cac  627
Ala Ser Asn Asn Ile Met Phe Lys Leu Asp Gly Cys Arg Asp Thr His
190                 195                 200                 205

cgc tac atc tgg atc aaa tac ttc aat ctg ttc gac aaa gaa ctg aac  675
Arg Tyr Ile Trp Ile Lys Tyr Phe Asn Leu Phe Asp Lys Glu Leu Asn
                210                 215                 220

gaa aaa gaa atc aaa gac ctg tac gac aac cag tcc aat tct ggt atc  723
Glu Lys Glu Ile Lys Asp Leu Tyr Asp Asn Gln Ser Asn Ser Gly Ile
            225                 230                 235

ctg aaa gac ttc tgg ggt gac tac ctg cag tac gac aaa ccg tac tac  771
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Leu Lys Asp Phe Trp Gly Asp Tyr Leu Gln Tyr Asp Lys Pro Tyr Tyr
        240                 245                 250

atg ctg aat ctg tac gat ccg aac aaa tac gtt gac gtc aac aat gta   819
Met Leu Asn Leu Tyr Asp Pro Asn Lys Tyr Val Asp Val Asn Asn Val
    255                 260                 265

ggt atc cgc ggt tac atg tac ctg aaa ggt ccg cgt ggt tct gtt atg   867
Gly Ile Arg Gly Tyr Met Tyr Leu Lys Gly Pro Arg Gly Ser Val Met
270                 275                 280                 285

act acc aac atc tac ctg aac tct tcc ctg tac cgt ggt acc aaa ttc   915
Thr Thr Asn Ile Tyr Leu Asn Ser Ser Leu Tyr Arg Gly Thr Lys Phe
                290                 295                 300

atc atc aag aaa tac gcg tct ggt aac aag gac aat atc gtt cgc aac   963
Ile Ile Lys Lys Tyr Ala Ser Gly Asn Lys Asp Asn Ile Val Arg Asn
            305                 310                 315

aat gat cgt gta tac atc aat gtt gta gtt aag aac aaa gaa tac cgt   1011
Asn Asp Arg Val Tyr Ile Asn Val Val Val Lys Asn Lys Glu Tyr Arg
        320                 325                 330

ctg gct acc aat gct tct cag gct ggt gta gaa aag atc ttg tct gct   1059
Leu Ala Thr Asn Ala Ser Gln Ala Gly Val Glu Lys Ile Leu Ser Ala
    335                 340                 345

ctg gaa atc ccg gac gtt ggt aat ctg tct cag gta gtt gta atg aaa   1107
Leu Glu Ile Pro Asp Val Gly Asn Leu Ser Gln Val Val Val Met Lys
350                 355                 360                 365

tcc aag aac gac cag ggt atc act aac aaa tgc aaa atg aat ctg cag   1155
Ser Lys Asn Asp Gln Gly Ile Thr Asn Lys Cys Lys Met Asn Leu Gln
                370                 375                 380

gac aac aat ggt aac gat atc ggt ttc atc ggt ttc cac cag ttc aac   1203
Asp Asn Asn Gly Asn Asp Ile Gly Phe Ile Gly Phe His Gln Phe Asn
            385                 390                 395

aat atc gct aaa ctg gtt gct tcc aac tgg tac aat cgt cag atc gaa   1251
Asn Ile Ala Lys Leu Val Ala Ser Asn Trp Tyr Asn Arg Gln Ile Glu
        400                 405                 410

cgt tcc tct cgc act ctg ggt tgc tct tgg gag ttc atc ccg gtt gat   1299
Arg Ser Ser Arg Thr Leu Gly Cys Ser Trp Glu Phe Ile Pro Val Asp
    415                 420                 425

gac ggt tgg ggt gaa cgt ccg ctg taa gaattc                       1332
Asp Gly Trp Gly Glu Arg Pro Leu  *
430                 435
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<210> 2
<211> 437
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct based on Clostridium botulinum sequence

<400> 2

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Met Arg Leu Leu Ser Thr Phe Thr Glu Tyr Ile Lys Asn Ile Ile Asn
 1               5                  10                  15
Thr Ser Ile Leu Asn Leu Arg Tyr Glu Ser Asn His Leu Ile Asp Leu
            20                  25                  30
Ser Arg Tyr Ala Ser Lys Ile Asn Ile Gly Ser Lys Val Asn Phe Asp
        35                  40                  45
Pro Ile Asp Lys Asn Gln Ile Gln Leu Phe Asn Leu Glu Ser Ser Lys
    50                  55                  60
Ile Glu Val Ile Leu Lys Asn Ala Ile Val Tyr Asn Ser Met Tyr Glu
65                  70                  75                  80
Asn Phe Ser Thr Ser Phe Trp Ile Arg Ile Pro Lys Tyr Phe Asn Ser
                85                  90                  95
Ile Ser Leu Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met Glu Asn Asn
            100                 105                 110
Ser Gly Trp Lys Val Ser Leu Asn Tyr Gly Glu Ile Ile Trp Thr Leu
        115                 120                 125
Gln Asp Thr Gln Glu Ile Lys Gln Arg Val Val Phe Lys Tyr Ser Gln
    130                 135                 140
Met Ile Asn Ile Ser Asp Tyr Ile Asn Arg Trp Ile Phe Val Thr Ile
145                 150                 155                 160
Thr Asn Asn Arg Leu Asn Asn Ser Lys Ile Tyr Ile Asn Gly Arg Leu
                165                 170                 175
Ile Asp Gln Lys Pro Ile Ser Asn Leu Gly Asn Ile His Ala Ser Asn
            180                 185                 190
Asn Ile Met Phe Lys Leu Asp Gly Cys Arg Asp Thr His Arg Tyr Ile
        195                 200                 205
Trp Ile Lys Tyr Phe Asn Leu Phe Asp Lys Glu Leu Asn Glu Lys Glu
    210                 215                 220
Ile Lys Asp Leu Tyr Asp Asn Gln Ser Asn Ser Gly Ile Leu Lys Asp
225                 230                 235                 240
Phe Trp Gly Asp Tyr Leu Gln Tyr Asp Lys Pro Tyr Tyr Met Leu Asn
                245                 250                 255
Leu Tyr Asp Pro Asn Lys Tyr Val Asp Val Asn Asn Val Gly Ile Arg
            260                 265                 270
Gly Tyr Met Tyr Leu Lys Gly Pro Arg Gly Ser Val Met Thr Thr Asn
        275                 280                 285
Ile Tyr Leu Asn Ser Ser Leu Tyr Arg Gly Thr Lys Phe Ile Ile Lys
    290                 295                 300
Lys Tyr Ala Ser Gly Asn Lys Asp Asn Ile Val Arg Asn Asn Asp Arg
305                 310                 315                 320
Val Tyr Ile Asn Val Val Val Lys Asn Lys Glu Tyr Arg Leu Ala Thr
                325                 330                 335
Asn Ala Ser Gln Ala Gly Val Glu Lys Ile Leu Ser Ala Leu Glu Ile
            340                 345                 350
Pro Asp Val Gly Asn Leu Ser Gln Val Val Val Met Lys Ser Lys Asn
        355                 360                 365
Asp Gln Gly Ile Thr Asn Lys Cys Lys Met Asn Leu Gln Asp Asn Asn
    370                 375                 380
Gly Asn Asp Ile Gly Phe Ile Gly Phe His Gln Phe Asn Asn Ile Ala
385                 390                 395                 400
Lys Leu Val Ala Ser Asn Trp Tyr Asn Arg Gln Ile Glu Arg Ser Ser
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                405                 410                 415
Arg Thr Leu Gly Cys Ser Trp Glu Phe Ile Pro Val Asp Asp Gly Trp
            420                 425                 430
Gly Glu Arg Pro Leu
        435
```

<210> 3
<211> 1323
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct based on Clostridium botulinum sequence

<221> CDS
<222> (13)...(1314)
<223> Synthetic Construct

<400> 3

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              Met Ser Thr Phe Thr Glu Tyr Ile Lys Asn Ile Ile Asn
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acc tcc atc ctg aac ctg cgc tac gaa tcc aat cac ctg atc gac ctg   99
Thr Ser Ile Leu Asn Leu Arg Tyr Glu Ser Asn His Leu Ile Asp Leu
     15                  20                  25

tct cgc tac gct tcc aaa atc aac atc ggt tct aaa gtt aac ttc gat   147
Ser Arg Tyr Ala Ser Lys Ile Asn Ile Gly Ser Lys Val Asn Phe Asp
 30                  35                  40                  45

ccg atc gac aag aat cag atc cag ctg ttc aat ctg gaa tct tcc aaa   195
Pro Ile Asp Lys Asn Gln Ile Gln Leu Phe Asn Leu Glu Ser Ser Lys
                 50                  55                  60

atc gaa gtt atc ctg aag aat gct atc gta tac aac tct atg tac gaa   243
Ile Glu Val Ile Leu Lys Asn Ala Ile Val Tyr Asn Ser Met Tyr Glu
             65                  70                  75

aac ttc tcc acc tcc ttc tgg atc cgt atc ccg aaa tac ttc aac tcc   291
Asn Phe Ser Thr Ser Phe Trp Ile Arg Ile Pro Lys Tyr Phe Asn Ser
         80                  85                  90

atc tct ctg aac aat gaa tac acc atc atc aac tgc atg gaa aac aat   339
Ile Ser Leu Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met Glu Asn Asn
     95                  100                 105

tct ggt tgg aaa gta tct ctg aac tac ggt gaa atc atc tgg act ctg   387
Ser Gly Trp Lys Val Ser Leu Asn Tyr Gly Glu Ile Ile Trp Thr Leu
110                 115                 120                 125

cag gac act cag gaa atc aaa cag cgt gtt gta ttc aaa tac tct cag   435
Gln Asp Thr Gln Glu Ile Lys Gln Arg Val Val Phe Lys Tyr Ser Gln
                130                 135                 140
```

```
atg atc aac atc tct gac tac atc aat cgc tgg atc ttc gtt acc atc   483
Met Ile Asn Ile Ser Asp Tyr Ile Asn Arg Trp Ile Phe Val Thr Ile
            145                 150                 155

acc aac aat cgt ctg aat aac tcc aaa atc tac atc aac ggc cgt ctg   531
Thr Asn Asn Arg Leu Asn Asn Ser Lys Ile Tyr Ile Asn Gly Arg Leu
        160                 165                 170

atc gac cag aaa ccg atc tcc aat ctg ggt aac atc cac gct tct aat   579
Ile Asp Gln Lys Pro Ile Ser Asn Leu Gly Asn Ile His Ala Ser Asn
    175                 180                 185

aac atc atg ttc aaa ctg gac ggt tgt cgt gac act cac cgc tac atc   627
Asn Ile Met Phe Lys Leu Asp Gly Cys Arg Asp Thr His Arg Tyr Ile
190                 195                 200                 205

tgg atc aaa tac ttc aat ctg ttc gac aaa gaa ctg aac gaa aaa gaa   675
Trp Ile Lys Tyr Phe Asn Leu Phe Asp Lys Glu Leu Asn Glu Lys Glu
                210                 215                 220

atc aaa gac ctg tac gac aac cag tcc aat tct ggt atc ctg aaa gac   723
Ile Lys Asp Leu Tyr Asp Asn Gln Ser Asn Ser Gly Ile Leu Lys Asp
            225                 230                 235

ttc tgg ggt gac tac ctg cag tac gac aaa ccg tac tac atg ctg aat   771
Phe Trp Gly Asp Tyr Leu Gln Tyr Asp Lys Pro Tyr Tyr Met Leu Asn
        240                 245                 250

ctg tac gat ccg aac aaa tac gtt gac gtc aac aat gta ggt atc cgc   819
Leu Tyr Asp Pro Asn Lys Tyr Val Asp Val Asn Asn Val Gly Ile Arg
    255                 260                 265

ggt tac atg tac ctg aaa ggt ccg cgt ggt tct gtt atg act acc aac   867
Gly Tyr Met Tyr Leu Lys Gly Pro Arg Gly Ser Val Met Thr Thr Asn
270                 275                 280                 285

atc tac ctg aac tct tcc ctg tac cgt ggt acc aaa ttc atc atc aag   915
Ile Tyr Leu Asn Ser Ser Leu Tyr Arg Gly Thr Lys Phe Ile Ile Lys
                290                 295                 300

aaa tac gcg tct ggt aac aag gac aat atc gtt cgc aac aat gat cgt   963
Lys Tyr Ala Ser Gly Asn Lys Asp Asn Ile Val Arg Asn Asn Asp Arg
            305                 310                 315

gta tac atc aat gtt gta gtt aag aac aaa gaa tac cgt ctg gct acc   1011
Val Tyr Ile Asn Val Val Val Lys Asn Lys Glu Tyr Arg Leu Ala Thr
        320                 325                 330

aat gct tct cag gct ggt gta gaa aag atc ttg tct gct ctg gaa atc   1059
Asn Ala Ser Gln Ala Gly Val Glu Lys Ile Leu Ser Ala Leu Glu Ile
    335                 340                 345

ccg gac gtt ggt aat ctg tct cag gta gtt gta atg aaa tcc aag aac   1107
Pro Asp Val Gly Asn Leu Ser Gln Val Val Val Met Lys Ser Lys Asn
350                 355                 360                 365
```

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gac cag ggt atc act aac aaa tgc aaa atg aat ctg cag gac aac aat   1155
Asp Gln Gly Ile Thr Asn Lys Cys Lys Met Asn Leu Gln Asp Asn Asn
                370                 375                 380

ggt aac gat atc ggt ttc atc ggt ttc cac cag ttc aac aat atc gct   1203
Gly Asn Asp Ile Gly Phe Ile Gly Phe His Gln Phe Asn Asn Ile Ala
            385                 390                 395

aaa ctg gtt gct tcc aac tgg tac aat cgt cag atc gaa cgt tcc tct   1251
Lys Leu Val Ala Ser Asn Trp Tyr Asn Arg Gln Ile Glu Arg Ser Ser
        400                 405                 410

cgc act ctg ggt tgc tct tgg gag ttc atc ccg gtt gat gac ggt tgg   1299
Arg Thr Leu Gly Cys Ser Trp Glu Phe Ile Pro Val Asp Asp Gly Trp
    415                 420                 425

ggt gaa cgt ccg ctg taagaattc                                    1323
Gly Glu Arg Pro Leu
430
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<210> 4
<211> 434
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct based on Clostridium botulinum sequence

<400> 4

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Met Ser Thr Phe Thr Glu Tyr Ile Lys Asn Ile Ile Asn Thr Ser Ile
 1               5                  10                  15
Leu Asn Leu Arg Tyr Glu Ser Asn His Leu Ile Asp Leu Ser Arg Tyr
            20                  25                  30
Ala Ser Lys Ile Asn Ile Gly Ser Lys Val Asn Phe Asp Pro Ile Asp
        35                  40                  45
Lys Asn Gln Ile Gln Leu Phe Asn Leu Glu Ser Ser Lys Ile Glu Val
    50                  55                  60
Ile Leu Lys Asn Ala Ile Val Tyr Asn Ser Met Tyr Glu Asn Phe Ser
65                  70                  75                  80
Thr Ser Phe Trp Ile Arg Ile Pro Lys Tyr Phe Asn Ser Ile Ser Leu
                85                  90                  95
Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met Glu Asn Asn Ser Gly Trp
            100                 105                 110
Lys Val Ser Leu Asn Tyr Gly Glu Ile Ile Trp Thr Leu Gln Asp Thr
        115                 120                 125
Gln Glu Ile Lys Gln Arg Val Val Phe Lys Tyr Ser Gln Met Ile Asn
    130                 135                 140
Ile Ser Asp Tyr Ile Asn Arg Trp Ile Phe Val Thr Ile Thr Asn Asn
145                 150                 155                 160
Arg Leu Asn Asn Ser Lys Ile Tyr Ile Asn Gly Arg Leu Ile Asp Gln
                165                 170                 175
Lys Pro Ile Ser Asn Leu Gly Asn Ile His Ala Ser Asn Asn Ile Met
            180                 185                 190
Phe Lys Leu Asp Gly Cys Arg Asp Thr His Arg Tyr Ile Trp Ile Lys
```

```
        195                 200                 205
Tyr Phe Asn Leu Phe Asp Lys Glu Leu Asn Glu Lys Glu Ile Lys Asp
    210                 215                 220
Leu Tyr Asp Asn Gln Ser Asn Ser Gly Ile Leu Lys Asp Phe Trp Gly
225                 230                 235                 240
Asp Tyr Leu Gln Tyr Asp Lys Pro Tyr Tyr Met Leu Asn Leu Tyr Asp
                245                 250                 255
Pro Asn Lys Tyr Val Asp Val Asn Asn Val Gly Ile Arg Gly Tyr Met
            260                 265                 270
Tyr Leu Lys Gly Pro Arg Gly Ser Val Met Thr Thr Asn Ile Tyr Leu
        275                 280                 285
Asn Ser Ser Leu Tyr Arg Gly Thr Lys Phe Ile Ile Lys Lys Tyr Ala
    290                 295                 300
Ser Gly Asn Lys Asp Asn Ile Val Arg Asn Asn Asp Arg Val Tyr Ile
305                 310                 315                 320
Asn Val Val Val Lys Asn Lys Glu Tyr Arg Leu Ala Thr Asn Ala Ser
                325                 330                 335
Gln Ala Gly Val Glu Lys Ile Leu Ser Ala Leu Glu Ile Pro Asp Val
            340                 345                 350
Gly Asn Leu Ser Gln Val Val Val Met Lys Ser Lys Asn Asp Gln Gly
        355                 360                 365
Ile Thr Asn Lys Cys Lys Met Asn Leu Gln Asp Asn Asn Gly Asn Asp
    370                 375                 380
Ile Gly Phe Ile Gly Phe His Gln Phe Asn Asn Ile Ala Lys Leu Val
385                 390                 395                 400
Ala Ser Asn Trp Tyr Asn Arg Gln Ile Glu Arg Ser Ser Arg Thr Leu
                405                 410                 415
Gly Cys Ser Trp Glu Phe Ile Pro Val Asp Asp Gly Trp Gly Glu Arg
            420                 425                 430
Pro Leu
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<210> 5
<211> 1326
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct based on Clostridium botulinum sequence

<220>
<221> CDS
<222> (13)...(1317)

<400> 5
gaattcgaaa cg atg gcc tct acc ttc act gaa tac atc aag aac atc atc 51
Met Ala Ser Thr Phe Thr Glu Tyr Ile Lys Asn Ile Ile
1 5 10

aat acc tcc atc ctg aac ctg cgc tac gaa tcc aat cac ctg atc gac 99
Asn Thr Ser Ile Leu Asn Leu Arg Tyr Glu Ser Asn His Leu Ile Asp
15 20 25

```
ctg tct cgc tac gct tcc aaa atc aac atc ggt tct aaa gtt aac ttc   147
Leu Ser Arg Tyr Ala Ser Lys Ile Asn Ile Gly Ser Lys Val Asn Phe
 30                  35                  40                  45

gat ccg atc gac aag aat cag atc cag ctg ttc aat ctg gaa tct tcc   195
Asp Pro Ile Asp Lys Asn Gln Ile Gln Leu Phe Asn Leu Glu Ser Ser
                50                  55                  60

aaa atc gaa gtt atc ctg aag aat gct atc gta tac aac tct atg tac   243
Lys Ile Glu Val Ile Leu Lys Asn Ala Ile Val Tyr Asn Ser Met Tyr
            65                  70                  75

gaa aac ttc tcc acc tcc ttc tgg atc cgt atc ccg aaa tac ttc aac   291
Glu Asn Phe Ser Thr Ser Phe Trp Ile Arg Ile Pro Lys Tyr Phe Asn
         80                  85                  90

tcc atc tct ctg aac aat gaa tac acc atc atc aac tgc atg gaa aac   339
Ser Ile Ser Leu Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met Glu Asn
     95                  100                 105

aat tct ggt tgg aaa gta tct ctg aac tac ggt gaa atc atc tgg act   387
Asn Ser Gly Trp Lys Val Ser Leu Asn Tyr Gly Glu Ile Ile Trp Thr
110                 115                 120                 125

ctg cag gac act cag gaa atc aaa cag cgt gtt gta ttc aaa tac tct   435
Leu Gln Asp Thr Gln Glu Ile Lys Gln Arg Val Val Phe Lys Tyr Ser
                130                 135                 140

cag atg atc aac atc tct gac tac atc aat cgc tgg atc ttc gtt acc   483
Gln Met Ile Asn Ile Ser Asp Tyr Ile Asn Arg Trp Ile Phe Val Thr
            145                 150                 155

atc acc aac aat cgt ctg aat aac tcc aaa atc tac atc aac ggc cgt   531
Ile Thr Asn Asn Arg Leu Asn Asn Ser Lys Ile Tyr Ile Asn Gly Arg
        160                 165                 170

ctg atc gac cag aaa ccg atc tcc aat ctg ggt aac atc cac gct tct   579
Leu Ile Asp Gln Lys Pro Ile Ser Asn Leu Gly Asn Ile His Ala Ser
    175                 180                 185

aat aac atc atg ttc aaa ctg gac ggt tgt cgt gac act cac cgc tac   627
Asn Asn Ile Met Phe Lys Leu Asp Gly Cys Arg Asp Thr His Arg Tyr
190                 195                 200                 205

atc tgg atc aaa tac ttc aat ctg ttc gac aaa gaa ctg aac gaa aaa   675
Ile Trp Ile Lys Tyr Phe Asn Leu Phe Asp Lys Glu Leu Asn Glu Lys
                210                 215                 220

gaa atc aaa gac ctg tac gac aac cag tcc aat tct ggt atc ctg aaa   723
Glu Ile Lys Asp Leu Tyr Asp Asn Gln Ser Asn Ser Gly Ile Leu Lys
            225                 230                 235

gac ttc tgg ggt gac tac ctg cag tac gac aaa ccg tac tac atg ctg   771
Asp Phe Trp Gly Asp Tyr Leu Gln Tyr Asp Lys Pro Tyr Tyr Met Leu
        240                 245                 250

aat ctg tac gat ccg aac aaa tac gtt gac gtc aac aat gta ggt atc   819
```

```
Asn Leu Tyr Asp Pro Asn Lys Tyr Val Asp Val Asn Asn Val Gly Ile
    255                 260                 265

cgc ggt tac atg tac ctg aaa ggt ccg cgt ggt tct gtt atg act acc   867
Arg Gly Tyr Met Tyr Leu Lys Gly Pro Arg Gly Ser Val Met Thr Thr
270                 275                 280                 285

aac atc tac ctg aac tct tcc ctg tac cgt ggt acc aaa ttc atc atc   915
Asn Ile Tyr Leu Asn Ser Ser Leu Tyr Arg Gly Thr Lys Phe Ile Ile
                290                 295                 300

aag aaa tac gcg tct ggt aac aag gac aat atc gtt cgc aac aat gat   963
Lys Lys Tyr Ala Ser Gly Asn Lys Asp Asn Ile Val Arg Asn Asn Asp
            305                 310                 315

cgt gta tac atc aat gtt gta gtt aag aac aaa gaa tac cgt ctg gct   1011
Arg Val Tyr Ile Asn Val Val Val Lys Asn Lys Glu Tyr Arg Leu Ala
        320                 325                 330

acc aat gct tct cag gct ggt gta gaa aag atc ttg tct gct ctg gaa   1059
Thr Asn Ala Ser Gln Ala Gly Val Glu Lys Ile Leu Ser Ala Leu Glu
    335                 340                 345

atc ccg gac gtt ggt aat ctg tct cag gta gtt gta atg aaa tcc aag   1107
Ile Pro Asp Val Gly Asn Leu Ser Gln Val Val Val Met Lys Ser Lys
350                 355                 360                 365

aac gac cag ggt atc act aac aaa tgc aaa atg aat ctg cag gac aac   1155
Asn Asp Gln Gly Ile Thr Asn Lys Cys Lys Met Asn Leu Gln Asp Asn
                370                 375                 380

aat ggt aac gat atc ggt ttc atc ggt ttc cac cag ttc aac aat atc   1203
Asn Gly Asn Asp Ile Gly Phe Ile Gly Phe His Gln Phe Asn Asn Ile
            385                 390                 395

gct aaa ctg gtt gct tcc aac tgg tac aat cgt cag atc gaa cgt tcc   1251
Ala Lys Leu Val Ala Ser Asn Trp Tyr Asn Arg Gln Ile Glu Arg Ser
        400                 405                 410

tct cgc act ctg ggt tgc tct tgg gag ttc atc ccg gtt gat gac ggt   1299
Ser Arg Thr Leu Gly Cys Ser Trp Glu Phe Ile Pro Val Asp Asp Gly
    415                 420                 425

tgg ggt gaa cgt ccg ctg taagaattc                                1326
Trp Gly Glu Arg Pro Leu
430                 435
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<210> 6
<211> 435
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct based on Clostridium botulinum sequence

<400> 6

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Met Ala Ser Thr Phe Thr Glu Tyr Ile Lys Asn Ile Ile Asn Thr Ser
 1               5                  10                  15
Ile Leu Asn Leu Arg Tyr Glu Ser Asn His Leu Ile Asp Leu Ser Arg
            20                  25                  30
Tyr Ala Ser Lys Ile Asn Ile Gly Ser Lys Val Asn Phe Asp Pro Ile
        35                  40                  45
Asp Lys Asn Gln Ile Gln Leu Phe Asn Leu Glu Ser Ser Lys Ile Glu
    50                  55                  60
Val Ile Leu Lys Asn Ala Ile Val Tyr Asn Ser Met Tyr Glu Asn Phe
65                  70                  75                  80
Ser Thr Ser Phe Trp Ile Arg Ile Pro Lys Tyr Phe Asn Ser Ile Ser
                85                  90                  95
Leu Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met Glu Asn Asn Ser Gly
            100                 105                 110
Trp Lys Val Ser Leu Asn Tyr Gly Glu Ile Ile Trp Thr Leu Gln Asp
        115                 120                 125
Thr Gln Glu Ile Lys Gln Arg Val Val Phe Lys Tyr Ser Gln Met Ile
    130                 135                 140
Asn Ile Ser Asp Tyr Ile Asn Arg Trp Ile Phe Val Thr Ile Thr Asn
145                 150                 155                 160
Asn Arg Leu Asn Asn Ser Lys Ile Tyr Ile Asn Gly Arg Leu Ile Asp
                165                 170                 175
Gln Lys Pro Ile Ser Asn Leu Gly Asn Ile His Ala Ser Asn Asn Ile
            180                 185                 190
Met Phe Lys Leu Asp Gly Cys Arg Asp Thr His Arg Tyr Ile Trp Ile
        195                 200                 205
Lys Tyr Phe Asn Leu Phe Asp Lys Glu Leu Asn Glu Lys Glu Ile Lys
    210                 215                 220
Asp Leu Tyr Asp Asn Gln Ser Asn Ser Gly Ile Leu Lys Asp Phe Trp
225                 230                 235                 240
Gly Asp Tyr Leu Gln Tyr Asp Lys Pro Tyr Tyr Met Leu Asn Leu Tyr
                245                 250                 255
Asp Pro Asn Lys Tyr Val Asp Val Asn Asn Val Gly Ile Arg Gly Tyr
            260                 265                 270
Met Tyr Leu Lys Gly Pro Arg Gly Ser Val Met Thr Thr Asn Ile Tyr
        275                 280                 285
Leu Asn Ser Ser Leu Tyr Arg Gly Thr Lys Phe Ile Ile Lys Lys Tyr
    290                 295                 300
Ala Ser Gly Asn Lys Asp Asn Ile Val Arg Asn Asn Asp Arg Val Tyr
305                 310                 315                 320
Ile Asn Val Val Val Lys Asn Lys Glu Tyr Arg Leu Ala Thr Asn Ala
                325                 330                 335
Ser Gln Ala Gly Val Glu Lys Ile Leu Ser Ala Leu Glu Ile Pro Asp
            340                 345                 350
Val Gly Asn Leu Ser Gln Val Val Val Met Lys Ser Lys Asn Asp Gln
        355                 360                 365
Gly Ile Thr Asn Lys Cys Lys Met Asn Leu Gln Asp Asn Asn Gly Asn
    370                 375                 380
Asp Ile Gly Phe Ile Gly Phe His Gln Phe Asn Asn Ile Ala Lys Leu
385                 390                 395                 400
Val Ala Ser Asn Trp Tyr Asn Arg Gln Ile Glu Arg Ser Ser Arg Thr
                405                 410                 415
Leu Gly Cys Ser Trp Glu Phe Ile Pro Val Asp Asp Gly Trp Gly Glu
            420                 425                 430
Arg Pro Leu
```

<210> 7
<211> 1341
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct based on Clostridium botulinum sequence

<221> CDS
<222> (10)...(1329)

<400> 7

```
gaattcacg atg gcc aac aaa tac aat tcc gaa atc ctg aac aat atc atc 51
          Met Ala Asn Lys Tyr Asn Ser Glu Ile Leu Asn Asn Ile Ile
           1               5                  10

ctg aac ctg cgt tac aaa gac aac aat ctg atc gat ctg tct ggt tac   99
Leu Asn Leu Arg Tyr Lys Asp Asn Asn Leu Ile Asp Leu Ser Gly Tyr
 15                  20                  25                  30

ggt gct aaa gtt gaa gta tac gac ggt gtt gaa ctg aat gac aag aac   147
Gly Ala Lys Val Glu Val Tyr Asp Gly Val Glu Leu Asn Asp Lys Asn
                 35                  40                  45

cag ttc aaa ctg acc tct tcc gct aac tct aag atc cgt gtt act cag   195
Gln Phe Lys Leu Thr Ser Ser Ala Asn Ser Lys Ile Arg Val Thr Gln
             50                  55                  60

aat cag aac atc atc ttc aac tcc gta ttc ctg gac ttc tct gtt tcc   243
Asn Gln Asn Ile Ile Phe Asn Ser Val Phe Leu Asp Phe Ser Val Ser
         65                  70                  75

ttc tgg att cgt atc ccg aaa tac aag aac gac ggt atc cag aat tac   291
Phe Trp Ile Arg Ile Pro Lys Tyr Lys Asn Asp Gly Ile Gln Asn Tyr
     80                  85                  90

atc cac aat gaa tac acc atc atc aac tgc atg aag aat aac tct ggt   339
Ile His Asn Glu Tyr Thr Ile Ile Asn Cys Met Lys Asn Asn Ser Gly
 95                  100                 105                 110

tgg aag atc tcc atc cgc ggt aac cgt atc atc tgg act ctg atc gat   387
Trp Lys Ile Ser Ile Arg Gly Asn Arg Ile Ile Trp Thr Leu Ile Asp
                115                 120                 125

atc aac ggt aag acc aaa tct gta ttc ttc gaa tac aac atc cgt gaa   435
Ile Asn Gly Lys Thr Lys Ser Val Phe Phe Glu Tyr Asn Ile Arg Glu
            130                 135                 140

gac atc tct gaa tac atc aat cgc tgg ttc ttc gtt acc atc acc aat   483
Asp Ile Ser Glu Tyr Ile Asn Arg Trp Phe Phe Val Thr Ile Thr Asn
        145                 150                 155
```

```
aac ctg aac aat gct aaa atc tac atc aac ggt aaa ctg gaa tct aat   531
Asn Leu Asn Asn Ala Lys Ile Tyr Ile Asn Gly Lys Leu Glu Ser Asn
    160                 165                 170

acc gac atc aaa gac atc cgt gaa gtt atc gct aac ggt gaa atc atc   579
Thr Asp Ile Lys Asp Ile Arg Glu Val Ile Ala Asn Gly Glu Ile Ile
175                 180                 185                 190

ttc aaa ctg gac ggt gac atc gat cgt acc cag ttc atc tgg atg aaa   627
Phe Lys Leu Asp Gly Asp Ile Asp Arg Thr Gln Phe Ile Trp Met Lys
                195                 200                 205

tac ttc tcc atc ttc aac acc gaa ctg tct cag tcc aat atc gaa gaa   675
Tyr Phe Ser Ile Phe Asn Thr Glu Leu Ser Gln Ser Asn Ile Glu Glu
            210                 215                 220

cgg tac aag atc cag tct tac tcc gaa tac ctg aaa gac ttc tgg ggt   723
Arg Tyr Lys Ile Gln Ser Tyr Ser Glu Tyr Leu Lys Asp Phe Trp Gly
        225                 230                 235

aat ccg ctg atg tac aac aaa gaa tac tat atg ttc aat gct ggt aac   771
Asn Pro Leu Met Tyr Asn Lys Glu Tyr Tyr Met Phe Asn Ala Gly Asn
    240                 245                 250

aag aac tct tac atc aaa ctg aag aaa gac tct ccg gtt ggt gaa atc   819
Lys Asn Ser Tyr Ile Lys Leu Lys Lys Asp Ser Pro Val Gly Glu Ile
255                 260                 265                 270

ctg act cgt tcc aaa tac aac cag aac tct aaa tac atc aac tac cgc   867
Leu Thr Arg Ser Lys Tyr Asn Gln Asn Ser Lys Tyr Ile Asn Tyr Arg
                275                 280                 285

gac ctg tac atc ggt gaa aag ttc atc atc cgt cgc aaa tct aac tct   915
Asp Leu Tyr Ile Gly Glu Lys Phe Ile Ile Arg Arg Lys Ser Asn Ser
            290                 295                 300

cag tcc atc aat gat gac atc gta cgt aaa gaa gac tac atc tac ctg   963
Gln Ser Ile Asn Asp Asp Ile Val Arg Lys Glu Asp Tyr Ile Tyr Leu
        305                 310                 315

gac ttc ttc aac ctg aat cag gaa tgg cgt gta tac acc tac aag tac   1011
Asp Phe Phe Asn Leu Asn Gln Glu Trp Arg Val Tyr Thr Tyr Lys Tyr
    320                 325                 330

ttc aag aaa gaa gaa gaa aag ctt ttc ctg gct ccg atc tct gat tcc   1059
Phe Lys Lys Glu Glu Glu Lys Leu Phe Leu Ala Pro Ile Ser Asp Ser
335                 340                 345                 350

gac gaa ctc tac aac acc atc cag atc aaa gaa tac gac gaa cag ccg   1107
Asp Glu Leu Tyr Asn Thr Ile Gln Ile Lys Glu Tyr Asp Glu Gln Pro
                355                 360                 365

acc tac tct tgc cag ctg ctg ttc aag aaa gat gaa gaa tct act gac   1155
Thr Tyr Ser Cys Gln Leu Leu Phe Lys Lys Asp Glu Glu Ser Thr Asp
            370                 375                 380

gaa atc ggt ctg atc ggt atc cac cgt ttc tac gaa tct ggt atc gta   1203
```

```
Glu Ile Gly Leu Ile Gly Ile His Arg Phe Tyr Glu Ser Gly Ile Val
        385                 390                 395

ttc gaa gaa tac aaa gac tac ttc tgc atc tcc aaa tgg tac ctg aag   1251
Phe Glu Glu Tyr Lys Asp Tyr Phe Cys Ile Ser Lys Trp Tyr Leu Lys
    400                 405                 410

gaa gtt aaa cgc aaa ccg tac aac ctg aaa ctg ggt tgc aat tgg cag   1299
Glu Val Lys Arg Lys Pro Tyr Asn Leu Lys Leu Gly Cys Asn Trp Gln
415                 420                 425                 430

ttc atc ccg aaa gac gaa ggt tgg acc gaa tagtaagaat tc             1341
Phe Ile Pro Lys Asp Glu Gly Trp Thr Glu
                435                 440
```

<210> 8
<211> 440
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct based on Clostridium botulinum sequence

<400> 8

```
Met Ala Asn Lys Tyr Asn Ser Glu Ile Leu Asn Asn Ile Ile Leu Asn
 1               5                  10                  15
Leu Arg Tyr Lys Asp Asn Asn Leu Ile Asp Leu Ser Gly Tyr Gly Ala
            20                  25                  30
Lys Val Glu Val Tyr Asp Gly Val Glu Leu Asn Asp Lys Asn Gln Phe
        35                  40                  45
Lys Leu Thr Ser Ser Ala Asn Ser Lys Ile Arg Val Thr Gln Asn Gln
    50                  55                  60
Asn Ile Ile Phe Asn Ser Val Phe Leu Asp Phe Ser Val Ser Phe Trp
65                  70                  75                  80
Ile Arg Ile Pro Lys Tyr Lys Asn Asp Gly Ile Gln Asn Tyr Ile His
                85                  90                  95
Asn Glu Tyr Thr Ile Ile Asn Cys Met Lys Asn Asn Ser Gly Trp Lys
            100                 105                 110
Ile Ser Ile Arg Gly Asn Arg Ile Ile Trp Thr Leu Ile Asp Ile Asn
        115                 120                 125
Gly Lys Thr Lys Ser Val Phe Phe Glu Tyr Asn Ile Arg Glu Asp Ile
    130                 135                 140
Ser Glu Tyr Ile Asn Arg Trp Phe Phe Val Thr Ile Thr Asn Asn Leu
145                 150                 155                 160
Asn Asn Ala Lys Ile Tyr Ile Asn Gly Lys Leu Glu Ser Asn Thr Asp
                165                 170                 175
Ile Lys Asp Ile Arg Glu Val Ile Ala Asn Gly Glu Ile Ile Phe Lys
            180                 185                 190
Leu Asp Gly Asp Ile Asp Arg Thr Gln Phe Ile Trp Met Lys Tyr Phe
        195                 200                 205
Ser Ile Phe Asn Thr Glu Leu Ser Gln Ser Asn Ile Glu Glu Arg Tyr
    210                 215                 220
Lys Ile Gln Ser Tyr Ser Glu Tyr Leu Lys Asp Phe Trp Gly Asn Pro
225                 230                 235                 240
```

```
Leu Met Tyr Asn Lys Glu Tyr Tyr Met Phe Asn Ala Gly Asn Lys Asn
                245                 250                 255
Ser Tyr Ile Lys Leu Lys Lys Asp Ser Pro Val Gly Glu Ile Leu Thr
            260                 265                 270
Arg Ser Lys Tyr Asn Gln Asn Ser Lys Tyr Ile Asn Tyr Arg Asp Leu
        275                 280                 285
Tyr Ile Gly Glu Lys Phe Ile Ile Arg Arg Lys Ser Asn Ser Gln Ser
    290                 295                 300
Ile Asn Asp Asp Ile Val Arg Lys Glu Asp Tyr Ile Tyr Leu Asp Phe
305                 310                 315                 320
Phe Asn Leu Asn Gln Glu Trp Arg Val Tyr Thr Tyr Lys Tyr Phe Lys
                325                 330                 335
Lys Glu Glu Glu Lys Leu Phe Leu Ala Pro Ile Ser Asp Ser Asp Glu
            340                 345                 350
Leu Tyr Asn Thr Ile Gln Ile Lys Glu Tyr Asp Glu Gln Pro Thr Tyr
        355                 360                 365
Ser Cys Gln Leu Leu Phe Lys Lys Asp Glu Glu Ser Thr Asp Glu Ile
    370                 375                 380
Gly Leu Ile Gly Ile His Arg Phe Tyr Glu Ser Gly Ile Val Phe Glu
385                 390                 395                 400
Glu Tyr Lys Asp Tyr Phe Cys Ile Ser Lys Trp Tyr Leu Lys Glu Val
                405                 410                 415
Lys Arg Lys Pro Tyr Asn Leu Lys Leu Gly Cys Asn Trp Gln Phe Ile
            420                 425                 430
Pro Lys Asp Glu Gly Trp Thr Glu
        435                 440
```

<210> 9
<211> 1371
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct based on Clostridium botulinum sequence

<221> CDS
<222> (10)...(1359)

<400> 9

```
gaattcacg atg acc atc cca ttc aac atc ttc tcc tac acc aac aac tcc 51
          Met Thr Ile Pro Phe Asn Ile Phe Ser Tyr Thr Asn Asn Ser
           1               5                   10

ctg ttg aag gac atc atc aac gag tac ttc aac aac atc aac gac tcc   99
Leu Leu Lys Asp Ile Ile Asn Glu Tyr Phe Asn Asn Ile Asn Asp Ser
 15                  20                  25                  30

aag atc ctg tcc ctg cag aac cgt aag aac acc ttg gtc gac acc tcc   147
Lys Ile Leu Ser Leu Gln Asn Arg Lys Asn Thr Leu Val Asp Thr Ser
                 35                  40                  45

ggt tac aac gcc gag gtc tcc gag gag ggt gac gtc cag ctg aac cca   195
Gly Tyr Asn Ala Glu Val Ser Glu Glu Gly Asp Val Gln Leu Asn Pro
             50                  55                  60
```

```
atc ttc cca ttc gac ttc aag ctg ggt tcc tcc ggt gag gac aga ggt   243
Ile Phe Pro Phe Asp Phe Lys Leu Gly Ser Ser Gly Glu Asp Arg Gly
         65                  70                  75

aag gtc atc gtc acc cag aac gag aac atc gtc tac aac tcc atg tac   291
Lys Val Ile Val Thr Gln Asn Glu Asn Ile Val Tyr Asn Ser Met Tyr
     80                  85                  90

gag tcc ttc tcc atc tcc ttc tgg atc aga atc aac aag tgg gtc tcc   339
Glu Ser Phe Ser Ile Ser Phe Trp Ile Arg Ile Asn Lys Trp Val Ser
 95                 100                 105                 110

aac ttg cca ggt tac acc atc atc gac tcc gtc aag aac aac tcc ggt   387
Asn Leu Pro Gly Tyr Thr Ile Ile Asp Ser Val Lys Asn Asn Ser Gly
                115                 120                 125

tgg tcc atc ggt atc atc tcc aac ttc ctg gtc ttc acc ctg aag cag   435
Trp Ser Ile Gly Ile Ile Ser Asn Phe Leu Val Phe Thr Leu Lys Gln
            130                 135                 140

aac gag gac tcc gag cag tcc atc aac ttc tcc tac gac atc tcc aac   483
Asn Glu Asp Ser Glu Gln Ser Ile Asn Phe Ser Tyr Asp Ile Ser Asn
        145                 150                 155

aac gct cct ggt tac aac aag tgg ttc ttc gtc acc gtc acc aac aac   531
Asn Ala Pro Gly Tyr Asn Lys Trp Phe Phe Val Thr Val Thr Asn Asn
    160                 165                 170

atg atg ggt aac atg aag atc tac atc aac ggt aag ctg atc gac acc   579
Met Met Gly Asn Met Lys Ile Tyr Ile Asn Gly Lys Leu Ile Asp Thr
175                 180                 185                 190

atc aag gtc aag gag ttg acc ggt atc aac ttc tcc aag acc atc acc   627
Ile Lys Val Lys Glu Leu Thr Gly Ile Asn Phe Ser Lys Thr Ile Thr
                195                 200                 205

ttc gag atc aac aag atc cca gac acc ggt ctg atc acc tcc gac tcc   675
Phe Glu Ile Asn Lys Ile Pro Asp Thr Gly Leu Ile Thr Ser Asp Ser
            210                 215                 220

gac aac atc aac atg tgg atc cgt gac ttc tac atc ttc gcc aag gag   723
Asp Asn Ile Asn Met Trp Ile Arg Asp Phe Tyr Ile Phe Ala Lys Glu
        225                 230                 235

ttg gac ggt aag gac atc aac atc ctg ttc aac tcc ttg cag tac acc   771
Leu Asp Gly Lys Asp Ile Asn Ile Leu Phe Asn Ser Leu Gln Tyr Thr
    240                 245                 250

aac gtc gtc aag gac tac tgg ggt aac gac ctg aga tac aac aag gag   819
Asn Val Val Lys Asp Tyr Trp Gly Asn Asp Leu Arg Tyr Asn Lys Glu
255                 260                 265                 270

tac tac atg gtc aac atc gac tac ttg aac aga tac atg tac gcc aac   867
Tyr Tyr Met Val Asn Ile Asp Tyr Leu Asn Arg Tyr Met Tyr Ala Asn
                275                 280                 285
```

```
tcc aga cag atc gtc ttc aac acc aga cgt aac aac aac gac ttc aac   915
Ser Arg Gln Ile Val Phe Asn Thr Arg Arg Asn Asn Asn Asp Phe Asn
            290                 295                 300

gag ggt tac aag atc atc atc aag cgt atc aga ggt aac acc aac gac   963
Glu Gly Tyr Lys Ile Ile Ile Lys Arg Ile Arg Gly Asn Thr Asn Asp
        305                 310                 315

acc aga gtc aga ggt ggt gac atc ctg tac ttc gac atg act atc aac   1011
Thr Arg Val Arg Gly Gly Asp Ile Leu Tyr Phe Asp Met Thr Ile Asn
    320                 325                 330

aac aag gcc tac aac ctg ttc atg aag aac gag acc atg tac gcc gac   1059
Asn Lys Ala Tyr Asn Leu Phe Met Lys Asn Glu Thr Met Tyr Ala Asp
335                 340                 345                 350

aac cac tcc acc gag gac atc tac gcc atc ggt ctg cgt gag cag acc   1107
Asn His Ser Thr Glu Asp Ile Tyr Ala Ile Gly Leu Arg Glu Gln Thr
                355                 360                 365

aag gac atc aac gac aac atc atc ttc cag atc cag cca atg aac aac   1155
Lys Asp Ile Asn Asp Asn Ile Ile Phe Gln Ile Gln Pro Met Asn Asn
            370                 375                 380

act tac tac tac gct tcc cag atc ttc aag tcc aac ttc aac ggt gag   1203
Thr Tyr Tyr Tyr Ala Ser Gln Ile Phe Lys Ser Asn Phe Asn Gly Glu
        385                 390                 395

aac atc tcc ggt atc tgt tcc atc ggt acc tac aga ttc cgt ctg ggt   1251
Asn Ile Ser Gly Ile Cys Ser Ile Gly Thr Tyr Arg Phe Arg Leu Gly
    400                 405                 410

ggt gac tgg tac aga cac aac tac ttg gtt cca act gtc aag cag ggt   1299
Gly Asp Trp Tyr Arg His Asn Tyr Leu Val Pro Thr Val Lys Gln Gly
415                 420                 425                 430

aac tac gcc tcc ttg ctg gag tcc act tcc acc cac tgg gga ttc gtc   1347
Asn Tyr Ala Ser Leu Leu Glu Ser Thr Ser Thr His Trp Gly Phe Val
                435                 440                 445

cca gtc tcc gag taataggaat tc                                    1371
Pro Val Ser Glu
            450
```

<210> 10
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct based on Clostridium botulinum sequence

<400> 10
Met Thr Ile Pro Phe Asn Ile Phe Ser Tyr Thr Asn Asn Ser Leu Leu

```
 1               5                  10                  15
Lys Asp Ile Ile Asn Glu Tyr Phe Asn Asn Ile Asn Asp Ser Lys Ile
            20                  25                  30
Leu Ser Leu Gln Asn Arg Lys Asn Thr Leu Val Asp Thr Ser Gly Tyr
        35                  40                  45
Asn Ala Glu Val Ser Glu Glu Gly Asp Val Gln Leu Asn Pro Ile Phe
    50                  55                  60
Pro Phe Asp Phe Lys Leu Gly Ser Ser Gly Glu Asp Arg Gly Lys Val
65                  70                  75                  80
Ile Val Thr Gln Asn Glu Asn Ile Val Tyr Asn Ser Met Tyr Glu Ser
                85                  90                  95
Phe Ser Ile Ser Phe Trp Ile Arg Ile Asn Lys Trp Val Ser Asn Leu
            100                 105                 110
Pro Gly Tyr Thr Ile Ile Asp Ser Val Lys Asn Asn Ser Gly Trp Ser
        115                 120                 125
Ile Gly Ile Ile Ser Asn Phe Leu Val Phe Thr Leu Lys Gln Asn Glu
    130                 135                 140
Asp Ser Glu Gln Ser Ile Asn Phe Ser Tyr Asp Ile Ser Asn Asn Ala
145                 150                 155                 160
Pro Gly Tyr Asn Lys Trp Phe Phe Val Thr Val Thr Asn Asn Met Met
                165                 170                 175
Gly Asn Met Lys Ile Tyr Ile Asn Gly Lys Leu Ile Asp Thr Ile Lys
            180                 185                 190
Val Lys Glu Leu Thr Gly Ile Asn Phe Ser Lys Thr Ile Thr Phe Glu
        195                 200                 205
Ile Asn Lys Ile Pro Asp Thr Gly Leu Ile Thr Ser Asp Ser Asp Asn
    210                 215                 220
Ile Asn Met Trp Ile Arg Asp Phe Tyr Ile Phe Ala Lys Glu Leu Asp
225                 230                 235                 240
Gly Lys Asp Ile Asn Ile Leu Phe Asn Ser Leu Gln Tyr Thr Asn Val
                245                 250                 255
Val Lys Asp Tyr Trp Gly Asn Asp Leu Arg Tyr Asn Lys Glu Tyr Tyr
            260                 265                 270
Met Val Asn Ile Asp Tyr Leu Asn Arg Tyr Met Tyr Ala Asn Ser Arg
        275                 280                 285
Gln Ile Val Phe Asn Thr Arg Arg Asn Asn Asn Asp Phe Asn Glu Gly
    290                 295                 300
Tyr Lys Ile Ile Ile Lys Arg Ile Arg Gly Asn Thr Asn Asp Thr Arg
305                 310                 315                 320
Val Arg Gly Gly Asp Ile Leu Tyr Phe Asp Met Thr Ile Asn Asn Lys
                325                 330                 335
Ala Tyr Asn Leu Phe Met Lys Asn Glu Thr Met Tyr Ala Asp Asn His
            340                 345                 350
Ser Thr Glu Asp Ile Tyr Ala Ile Gly Leu Arg Glu Gln Thr Lys Asp
        355                 360                 365
Ile Asn Asp Asn Ile Ile Phe Gln Ile Gln Pro Met Asn Asn Thr Tyr
    370                 375                 380
Tyr Tyr Ala Ser Gln Ile Phe Lys Ser Asn Phe Asn Gly Glu Asn Ile
385                 390                 395                 400
Ser Gly Ile Cys Ser Ile Gly Thr Tyr Arg Phe Arg Leu Gly Gly Asp
                405                 410                 415
Trp Tyr Arg His Asn Tyr Leu Val Pro Thr Val Lys Gln Gly Asn Tyr
            420                 425                 430
Ala Ser Leu Leu Glu Ser Thr Ser Thr His Trp Gly Phe Val Pro Val
        435                 440                 445
Ser Glu
    450
```

<210> 11
<211> 1374
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct based on Clostridium botulinum sequence

<221> CDS
<222> (10)...(1362)

<400> 11
gaattcacg atg cgt ttg aag gct aag gtc aac gag tcc ttc gag aac acc 51
Met Arg Leu Lys Ala Lys Val Asn Glu Ser Phe Glu Asn Thr
1 5 10

atg cca ttc aac atc ttc tcc tac acc aac aac tcc ttg ttg aag gac 99
Met Pro Phe Asn Ile Phe Ser Tyr Thr Asn Asn Ser Leu Leu Lys Asp
15 20 25 30

atc atc aac gag tac ttc aac tcc atc aac gac tcc aag atc ttg tcc 147
Ile Ile Asn Glu Tyr Phe Asn Ser Ile Asn Asp Ser Lys Ile Leu Ser
35 40 45

ttg cag aac aag aag aac gcc ttg gtc gac acc tcc ggt tac aac gcc 195
Leu Gln Asn Lys Lys Asn Ala Leu Val Asp Thr Ser Gly Tyr Asn Ala
50 55 60

gag gtc aga gtc ggt gac aac gtc cag ttg aac acc atc tac acc aac 243
Glu Val Arg Val Gly Asp Asn Val Gln Leu Asn Thr Ile Tyr Thr Asn
65 70 75

gac ttc aag ttg tcc tct tcc ggt gac aag atc atc gtc aac ttg aac 291
Asp Phe Lys Leu Ser Ser Ser Gly Asp Lys Ile Ile Val Asn Leu Asn
80 85 90

aac aac atc ttg tac tcc gcc atc tac gag aac tcc tct gtc tcc ttc 339
Asn Asn Ile Leu Tyr Ser Ala Ile Tyr Glu Asn Ser Ser Val Ser Phe
95 100 105 110

tgg atc aag atc tcc aag gac ttg acc aac tcc cac aac gag tac acc 387
Trp Ile Lys Ile Ser Lys Asp Leu Thr Asn Ser His Asn Glu Tyr Thr
115 120 125

atc atc aac tcc atc gag cag aac tcc ggt tgg aag ttg tgt atc cgt 435
Ile Ile Asn Ser Ile Glu Gln Asn Ser Gly Trp Lys Leu Cys Ile Arg
130 135 140

aac ggt aac atc gag tgg atc ttg cag gac gtc aac cgt aag tac aag 483
Asn Gly Asn Ile Glu Trp Ile Leu Gln Asp Val Asn Arg Lys Tyr Lys
145 150 155

tcc ttg atc ttc gac tac tcc gag tcc ttg tcc cac acc ggt tac acc 531
Ser Leu Ile Phe Asp Tyr Ser Glu Ser Leu Ser His Thr Gly Tyr Thr

```
    160                 165                 170

aac aag tgg ttc ttc gtc acc atc acc aac aac atc atg ggt tac atg   579
Asn Lys Trp Phe Phe Val Thr Ile Thr Asn Asn Ile Met Gly Tyr Met
175                 180                 185                 190

aag ttg tac atc aac ggt gag ttg aag cag tcc cag aag atc gag gac   627
Lys Leu Tyr Ile Asn Gly Glu Leu Lys Gln Ser Gln Lys Ile Glu Asp
                195                 200                 205

ctg gac gag gtc aag ctg gac aag acc atc gtc ttc ggt atc gac gag   675
Leu Asp Glu Val Lys Leu Asp Lys Thr Ile Val Phe Gly Ile Asp Glu
            210                 215                 220

aac atc gac gag aac cag atg ttg tgg att cgt gac ttc aac atc ttc   723
Asn Ile Asp Glu Asn Gln Met Leu Trp Ile Arg Asp Phe Asn Ile Phe
        225                 230                 235

tcc aag gag ctg tcc aac gag gac atc aac atc gtc tac gag ggt cag   771
Ser Lys Glu Leu Ser Asn Glu Asp Ile Asn Ile Val Tyr Glu Gly Gln
    240                 245                 250

atc ctg agg aac gtc atc aag gac tac tgg ggt aac cca ctg aag ttc   819
Ile Leu Arg Asn Val Ile Lys Asp Tyr Trp Gly Asn Pro Leu Lys Phe
255                 260                 265                 270

gac acc gag tac tac atc atc aac gac aac tac atc gac cgt tac atc   867
Asp Thr Glu Tyr Tyr Ile Ile Asn Asp Asn Tyr Ile Asp Arg Tyr Ile
                275                 280                 285

gcc cca gag tcc aac gtc ctg gtc ctg gtc cag tac cct gac ctg tcc   915
Ala Pro Glu Ser Asn Val Leu Val Leu Val Gln Tyr Pro Asp Leu Ser
            290                 295                 300

aag ctg tac acc ggt aac cct atc acc atc aag tcc gtc tcc gac aag   963
Lys Leu Tyr Thr Gly Asn Pro Ile Thr Ile Lys Ser Val Ser Asp Lys
        305                 310                 315

aac cct tac tcc cgt atc ctg aac ggt gac aac atc atc ctg cac atg   1011
Asn Pro Tyr Ser Arg Ile Leu Asn Gly Asp Asn Ile Ile Leu His Met
    320                 325                 330

ctg tac aac tcc cgt aag tac atg atc atc cgt gac acc gac acc atc   1059
Leu Tyr Asn Ser Arg Lys Tyr Met Ile Ile Arg Asp Thr Asp Thr Ile
335                 340                 345                 350

tac gcc acc cag ggt ggt gag tgt tcc cag aac tgt gtc tac gcc ctg   1107
Tyr Ala Thr Gln Gly Gly Glu Cys Ser Gln Asn Cys Val Tyr Ala Leu
                355                 360                 365

aag ctg cag tcc aac ctg ggt aac tac ggt atc ggt atc ttc tcc atc   1155
Lys Leu Gln Ser Asn Leu Gly Asn Tyr Gly Ile Gly Ile Phe Ser Ile
            370                 375                 380

aag aac atc gtc tcc aag aac aag tac tgc tcc cag atc ttc tcc tcc   1203
Lys Asn Ile Val Ser Lys Asn Lys Tyr Cys Ser Gln Ile Phe Ser Ser
        385                 390                 395
```

```
ttc cgt gag aac acc atg ctg ctg gcc gac atc tac aag cct tgg cgt   1251
Phe Arg Glu Asn Thr Met Leu Leu Ala Asp Ile Tyr Lys Pro Trp Arg
    400                 405                 410

ttc tcc ttc aag aac gcc tac act cct gtc gcc gtc acc aac tac gag   1299
Phe Ser Phe Lys Asn Ala Tyr Thr Pro Val Ala Val Thr Asn Tyr Glu
415                 420                 425                 430

acc aag ctg ctg tcc acc tcc tcc ttc tgg aag ttc atc tcc cgt gac   1347
Thr Lys Leu Leu Ser Thr Ser Ser Phe Trp Lys Phe Ile Ser Arg Asp
                435                 440                 445

cca ggt tgg gtc gag taataggaat tc                                 1374
Pro Gly Trp Val Glu
            450
```

<210> 12
<211> 451
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 12

```
Met Arg Leu Lys Ala Lys Val Asn Glu Ser Phe Glu Asn Thr Met Pro
 1               5                  10                  15
Phe Asn Ile Phe Ser Tyr Thr Asn Asn Ser Leu Leu Lys Asp Ile Ile
            20                  25                  30
Asn Glu Tyr Phe Asn Ser Ile Asn Asp Ser Lys Ile Leu Ser Leu Gln
        35                  40                  45
Asn Lys Lys Asn Ala Leu Val Asp Thr Ser Gly Tyr Asn Ala Glu Val
    50                  55                  60
Arg Val Gly Asp Asn Val Gln Leu Asn Thr Ile Tyr Thr Asn Asp Phe
65                  70                  75                  80
Lys Leu Ser Ser Ser Gly Asp Lys Ile Ile Val Asn Leu Asn Asn Asn
                85                  90                  95
Ile Leu Tyr Ser Ala Ile Tyr Glu Asn Ser Ser Val Ser Phe Trp Ile
            100                 105                 110
Lys Ile Ser Lys Asp Leu Thr Asn Ser His Asn Glu Tyr Thr Ile Ile
        115                 120                 125
Asn Ser Ile Glu Gln Asn Ser Gly Trp Lys Leu Cys Ile Arg Asn Gly
    130                 135                 140
Asn Ile Glu Trp Ile Leu Gln Asp Val Asn Arg Lys Tyr Lys Ser Leu
145                 150                 155                 160
Ile Phe Asp Tyr Ser Glu Ser Leu Ser His Thr Gly Tyr Thr Asn Lys
                165                 170                 175
Trp Phe Phe Val Thr Ile Thr Asn Asn Ile Met Gly Tyr Met Lys Leu
            180                 185                 190
Tyr Ile Asn Gly Glu Leu Lys Gln Ser Gln Lys Ile Glu Asp Leu Asp
        195                 200                 205
Glu Val Lys Leu Asp Lys Thr Ile Val Phe Gly Ile Asp Glu Asn Ile
    210                 215                 220
Asp Glu Asn Gln Met Leu Trp Ile Arg Asp Phe Asn Ile Phe Ser Lys
225                 230                 235                 240
```

```
Glu Leu Ser Asn Glu Asp Ile Asn Ile Val Tyr Glu Gly Gln Ile Leu
                245                 250                 255
Arg Asn Val Ile Lys Asp Tyr Trp Gly Asn Pro Leu Lys Phe Asp Thr
            260                 265                 270
Glu Tyr Tyr Ile Ile Asn Asp Asn Tyr Ile Asp Arg Tyr Ile Ala Pro
        275                 280                 285
Glu Ser Asn Val Leu Val Leu Val Gln Tyr Pro Asp Leu Ser Lys Leu
    290                 295                 300
Tyr Thr Gly Asn Pro Ile Thr Ile Lys Ser Val Ser Asp Lys Asn Pro
305                 310                 315                 320
Tyr Ser Arg Ile Leu Asn Gly Asp Asn Ile Ile Leu His Met Leu Tyr
                325                 330                 335
Asn Ser Arg Lys Tyr Met Ile Ile Arg Asp Thr Asp Thr Ile Tyr Ala
            340                 345                 350
Thr Gln Gly Gly Glu Cys Ser Gln Asn Cys Val Tyr Ala Leu Lys Leu
        355                 360                 365
Gln Ser Asn Leu Gly Asn Tyr Gly Ile Gly Ile Phe Ser Ile Lys Asn
    370                 375                 380
Ile Val Ser Lys Asn Lys Tyr Cys Ser Gln Ile Phe Ser Ser Phe Arg
385                 390                 395                 400
Glu Asn Thr Met Leu Leu Ala Asp Ile Tyr Lys Pro Trp Arg Phe Ser
                405                 410                 415
Phe Lys Asn Ala Tyr Thr Pro Val Ala Val Thr Asn Tyr Glu Thr Lys
            420                 425                 430
Leu Leu Ser Thr Ser Ser Phe Trp Lys Phe Ile Ser Arg Asp Pro Gly
        435                 440                 445
Trp Val Glu
    450
```

<210> 13
<211> 1400
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct based on Clostridium botulinum sequence

<221> CDS
<222> (10)...(1356)

<400> 13

```
gaattcacc atg gga gag agt cag caa gaa cta aat tct atg gta act gat 51
          Met Gly Glu Ser Gln Gln Glu Leu Asn Ser Met Val Thr Asp
           1               5                   10

acc cta aat aat agt att cct ttt aag ctt tct tct tat aca gat gat   99
Thr Leu Asn Asn Ser Ile Pro Phe Lys Leu Ser Ser Tyr Thr Asp Asp
 15                  20                  25                  30

aaa att tta att tcc tac ttc aac aag ttc ttc aag aga att aag tct   147
Lys Ile Leu Ile Ser Tyr Phe Asn Lys Phe Phe Lys Arg Ile Lys Ser
                 35                  40                  45

tct tcc gtt tta aac atg aga tac aag aat gat aaa tac gtc gac act   195
Ser Ser Val Leu Asn Met Arg Tyr Lys Asn Asp Lys Tyr Val Asp Thr
```

```
            50                  55                  60

tcc ggt tac gac tcc aat atc aac att aac ggt gac gtg tac aag tac   243
Ser Gly Tyr Asp Ser Asn Ile Asn Ile Asn Gly Asp Val Tyr Lys Tyr
         65                  70                  75

cca act aac aaa aac caa ttc ggt atc tac aac gac aag ctt tcc gag   291
Pro Thr Asn Lys Asn Gln Phe Gly Ile Tyr Asn Asp Lys Leu Ser Glu
     80                  85                  90

gtc aac atc tct caa aac gac tac att atc tac gac aac aag tac aag   339
Val Asn Ile Ser Gln Asn Asp Tyr Ile Ile Tyr Asp Asn Lys Tyr Lys
 95                 100                 105                 110

aac ttc tct att tct ttc tgg gtc agg att cct aac tac gac aac aag   387
Asn Phe Ser Ile Ser Phe Trp Val Arg Ile Pro Asn Tyr Asp Asn Lys
                115                 120                 125

atc gtc aac gtt aac aac gag tac act atc atc aac tgt atg aga gac   435
Ile Val Asn Val Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met Arg Asp
            130                 135                 140

aac aac tcc ggt tgg aag gtc tct ctt aac cac aac gag atc att tgg   483
Asn Asn Ser Gly Trp Lys Val Ser Leu Asn His Asn Glu Ile Ile Trp
        145                 150                 155

acc ttg caa gac aac gca ggt att aac caa aag tta gca ttc aac tac   531
Thr Leu Gln Asp Asn Ala Gly Ile Asn Gln Lys Leu Ala Phe Asn Tyr
    160                 165                 170

ggt aac gca aac ggt att tct gac tac atc aac aag tgg att ttc gtc   579
Gly Asn Ala Asn Gly Ile Ser Asp Tyr Ile Asn Lys Trp Ile Phe Val
175                 180                 185                 190

act atc act aac gac aga tta ggt gac tct aag ctt tac att aac ggt   627
Thr Ile Thr Asn Asp Arg Leu Gly Asp Ser Lys Leu Tyr Ile Asn Gly
                195                 200                 205

aac tta atc gac caa aag tcc att tta aac tta ggt aac att cac gtt   675
Asn Leu Ile Asp Gln Lys Ser Ile Leu Asn Leu Gly Asn Ile His Val
            210                 215                 220

tct gac aac atc tta ttc aag atc gtt aac tgc agt tac acc aga tac   723
Ser Asp Asn Ile Leu Phe Lys Ile Val Asn Cys Ser Tyr Thr Arg Tyr
        225                 230                 235

att ggc att aga tac ttc aac att ttc gac aag gag tta gac gag acc   771
Ile Gly Ile Arg Tyr Phe Asn Ile Phe Asp Lys Glu Leu Asp Glu Thr
    240                 245                 250

gag att caa act tta tac agc aac gaa cct aac acc aat att ttg aag   819
Glu Ile Gln Thr Leu Tyr Ser Asn Glu Pro Asn Thr Asn Ile Leu Lys
255                 260                 265                 270

gac ttc tgg ggt aac tac ttg ctt tac gac aag gaa tac tac tta tta   867
Asp Phe Trp Gly Asn Tyr Leu Leu Tyr Asp Lys Glu Tyr Tyr Leu Leu
                275                 280                 285
```

```
aac gtg tta aag cca aac aac ttc att gat agg aga aag gat tct act   915
Asn Val Leu Lys Pro Asn Asn Phe Ile Asp Arg Arg Lys Asp Ser Thr
            290                 295                 300

tta agc att aac aac atc aga agc act att ctt tta gct aac aga tta   963
Leu Ser Ile Asn Asn Ile Arg Ser Thr Ile Leu Leu Ala Asn Arg Leu
        305                 310                 315

tac tct ggt atc aag gtt aag atc caa aga gtt aac aac tct tct act   1011
Tyr Ser Gly Ile Lys Val Lys Ile Gln Arg Val Asn Asn Ser Ser Thr
    320                 325                 330

aac gat aac ctt gtt aga aag aac gat cag gtc tat att aac ttc gtc   1059
Asn Asp Asn Leu Val Arg Lys Asn Asp Gln Val Tyr Ile Asn Phe Val
335                 340                 345                 350

gct agc aag act cac tta ttc cca tta tat gct gat acc gct acc acc   1107
Ala Ser Lys Thr His Leu Phe Pro Leu Tyr Ala Asp Thr Ala Thr Thr
                355                 360                 365

aac aag gag aag acc atc aag atc tcc tcc tct ggc aac aga ttt aac   1155
Asn Lys Glu Lys Thr Ile Lys Ile Ser Ser Ser Gly Asn Arg Phe Asn
            370                 375                 380

caa gtc gtc gtt atg aac tcc gtc ggt aac aac tgt acc atg aac ttt   1203
Gln Val Val Val Met Asn Ser Val Gly Asn Asn Cys Thr Met Asn Phe
        385                 390                 395

aaa aat aat aat gga aat aat att ggg ttg tta ggt ttc aag gca gat   1251
Lys Asn Asn Asn Gly Asn Asn Ile Gly Leu Leu Gly Phe Lys Ala Asp
    400                 405                 410

act gta gtt gct agt act tgg tat tat acc cac atg aga gat cac acc   1299
Thr Val Val Ala Ser Thr Trp Tyr Tyr Thr His Met Arg Asp His Thr
415                 420                 425                 430

aac agc aat gga tgt ttt tgg aac ttt att tct gaa gaa cat gga tgg   1347
Asn Ser Asn Gly Cys Phe Trp Asn Phe Ile Ser Glu Glu His Gly Trp
                435                 440                 445

caa gaa aaa taatagggat ccgcggccgc acgcgtcccg ggactagtga          1396
Gln Glu Lys

attc                                                             1400
```

<210> 14
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 14
Met Gly Glu Ser Gln Gln Glu Leu Asn Ser Met Val Thr Asp Thr Leu

```
 1               5                  10                  15
Asn Asn Ser Ile Pro Phe Lys Leu Ser Ser Tyr Thr Asp Asp Lys Ile
            20                  25                  30
Leu Ile Ser Tyr Phe Asn Lys Phe Phe Lys Arg Ile Lys Ser Ser Ser
        35                  40                  45
Val Leu Asn Met Arg Tyr Lys Asn Asp Lys Tyr Val Asp Thr Ser Gly
    50                  55                  60
Tyr Asp Ser Asn Ile Asn Ile Asn Gly Asp Val Tyr Lys Tyr Pro Thr
65                  70                  75                  80
Asn Lys Asn Gln Phe Gly Ile Tyr Asn Asp Lys Leu Ser Glu Val Asn
                85                  90                  95
Ile Ser Gln Asn Asp Tyr Ile Ile Tyr Asp Asn Lys Tyr Lys Asn Phe
            100                 105                 110
Ser Ile Ser Phe Trp Val Arg Ile Pro Asn Tyr Asp Asn Lys Ile Val
        115                 120                 125
Asn Val Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met Arg Asp Asn Asn
    130                 135                 140
Ser Gly Trp Lys Val Ser Leu Asn His Asn Glu Ile Ile Trp Thr Leu
145                 150                 155                 160
Gln Asp Asn Ala Gly Ile Asn Gln Lys Leu Ala Phe Asn Tyr Gly Asn
                165                 170                 175
Ala Asn Gly Ile Ser Asp Tyr Ile Asn Lys Trp Ile Phe Val Thr Ile
            180                 185                 190
Thr Asn Asp Arg Leu Gly Asp Ser Lys Leu Tyr Ile Asn Gly Asn Leu
        195                 200                 205
Ile Asp Gln Lys Ser Ile Leu Asn Leu Gly Asn Ile His Val Ser Asp
    210                 215                 220
Asn Ile Leu Phe Lys Ile Val Asn Cys Ser Tyr Thr Arg Tyr Ile Gly
225                 230                 235                 240
Ile Arg Tyr Phe Asn Ile Phe Asp Lys Glu Leu Asp Glu Thr Glu Ile
                245                 250                 255
Gln Thr Leu Tyr Ser Asn Glu Pro Asn Thr Asn Ile Leu Lys Asp Phe
            260                 265                 270
Trp Gly Asn Tyr Leu Leu Tyr Asp Lys Glu Tyr Tyr Leu Leu Asn Val
        275                 280                 285
Leu Lys Pro Asn Asn Phe Ile Asp Arg Arg Lys Asp Ser Thr Leu Ser
    290                 295                 300
Ile Asn Asn Ile Arg Ser Thr Ile Leu Leu Ala Asn Arg Leu Tyr Ser
305                 310                 315                 320
Gly Ile Lys Val Lys Ile Gln Arg Val Asn Asn Ser Ser Thr Asn Asp
                325                 330                 335
Asn Leu Val Arg Lys Asn Asp Gln Val Tyr Ile Asn Phe Val Ala Ser
            340                 345                 350
Lys Thr His Leu Phe Pro Leu Tyr Ala Asp Thr Ala Thr Thr Asn Lys
        355                 360                 365
Glu Lys Thr Ile Lys Ile Ser Ser Ser Gly Asn Arg Phe Asn Gln Val
    370                 375                 380
Val Val Met Asn Ser Val Gly Asn Asn Cys Thr Met Asn Phe Lys Asn
385                 390                 395                 400
Asn Asn Gly Asn Asn Ile Gly Leu Leu Gly Phe Lys Ala Asp Thr Val
                405                 410                 415
Val Ala Ser Thr Trp Tyr Tyr Thr His Met Arg Asp His Thr Asn Ser
            420                 425                 430
Asn Gly Cys Phe Trp Asn Phe Ile Ser Glu Glu His Gly Trp Gln Glu
        435                 440                 445
Lys
```

<210> 15
<211> 1317
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<221> CDS
<222> (10)...(1305)

<400> 15
```
gaattcacg atg tcc tac acc aac gac aag atc ctg atc ttg tac ttc aac 51
          Met Ser Tyr Thr Asn Asp Lys Ile Leu Ile Leu Tyr Phe Asn
           1               5                  10

aag ctg tac aag aag atc aag gac aac tcc atc ttg gac atg aga tac   99
Lys Leu Tyr Lys Lys Ile Lys Asp Asn Ser Ile Leu Asp Met Arg Tyr
 15                  20                  25                  30

gaa aac aat aag ttc atc gac atc tcc ggt tac ggt tcc aac atc tcc   147
Glu Asn Asn Lys Phe Ile Asp Ile Ser Gly Tyr Gly Ser Asn Ile Ser
                 35                  40                  45

atc aac ggt gac gtc tac atc tac tcc acc aat aga aac cag ttc gga   195
Ile Asn Gly Asp Val Tyr Ile Tyr Ser Thr Asn Arg Asn Gln Phe Gly
             50                  55                  60

atc tac tcc tcc aag cct tcc gag gtc aac atc gct cag aac aac gac   243
Ile Tyr Ser Ser Lys Pro Ser Glu Val Asn Ile Ala Gln Asn Asn Asp
         65                  70                  75

atc atc tac aac gga aga tac cag aac ttc tcc atc tcc ttc tgg gtc   291
Ile Ile Tyr Asn Gly Arg Tyr Gln Asn Phe Ser Ile Ser Phe Trp Val
     80                  85                  90

cgt atc cca aag tac ttc aac aag gtc aac ctg aat aac gag tac acc   339
Arg Ile Pro Lys Tyr Phe Asn Lys Val Asn Leu Asn Asn Glu Tyr Thr
 95                  100                 105                 110

atc atc gac tgc atc cgt aac aat aac tcc gga tgg aag atc tcc ctg   387
Ile Ile Asp Cys Ile Arg Asn Asn Asn Ser Gly Trp Lys Ile Ser Leu
                115                 120                 125

aac tac aac aag atc atc tgg acc ctg cag gac acc gcc ggt aac aat   435
Asn Tyr Asn Lys Ile Ile Trp Thr Leu Gln Asp Thr Ala Gly Asn Asn
            130                 135                 140

cag aag ttg gtc ttc aac tac acc cag atg atc tcc atc tcc gac tac   483
Gln Lys Leu Val Phe Asn Tyr Thr Gln Met Ile Ser Ile Ser Asp Tyr
        145                 150                 155

atc aac aag tgg atc ttc gtc acc atc acc aat aac cgt ttg gga aac   531
Ile Asn Lys Trp Ile Phe Val Thr Ile Thr Asn Asn Arg Leu Gly Asn
    160                 165                 170
```

```
tcc aga atc tac atc aac ggt aac ttg atc gac gag aag tcc atc tcc   579
Ser Arg Ile Tyr Ile Asn Gly Asn Leu Ile Asp Glu Lys Ser Ile Ser
175                 180                 185                 190

aac ttg ggt gac atc cac gtc tcc gac aac att ttg ttc aag atc gtc   627
Asn Leu Gly Asp Ile His Val Ser Asp Asn Ile Leu Phe Lys Ile Val
                195                 200                 205

ggt tgt aac gac acc cgt tac gtc ggg atc cgt tac ttc aaa gtc ttc   675
Gly Cys Asn Asp Thr Arg Tyr Val Gly Ile Arg Tyr Phe Lys Val Phe
            210                 215                 220

gac act gag ttg ggt aag acc gag atc gag acc ttg tac tcc gac gag   723
Asp Thr Glu Leu Gly Lys Thr Glu Ile Glu Thr Leu Tyr Ser Asp Glu
        225                 230                 235

cct gac cca tcc atc ctg aag gac ttc tgg ggt aac tac ctg ctg tac   771
Pro Asp Pro Ser Ile Leu Lys Asp Phe Trp Gly Asn Tyr Leu Leu Tyr
    240                 245                 250

aac aaa cgt tac tac ttg ctg aac ttg ttg cgt acc gac aag tcc atc   819
Asn Lys Arg Tyr Tyr Leu Leu Asn Leu Leu Arg Thr Asp Lys Ser Ile
255                 260                 265                 270

acc cag aac tcc aac ttc ttg aac atc aac cag cag aga ggt gtc tac   867
Thr Gln Asn Ser Asn Phe Leu Asn Ile Asn Gln Gln Arg Gly Val Tyr
                275                 280                 285

cag aag cca aac atc ttc tcc aac acc aga ttg tac acc gga gtc gag   915
Gln Lys Pro Asn Ile Phe Ser Asn Thr Arg Leu Tyr Thr Gly Val Glu
            290                 295                 300

gtc att atc aga aag aac gga tct act gat att tcc aac acc gat aac   963
Val Ile Ile Arg Lys Asn Gly Ser Thr Asp Ile Ser Asn Thr Asp Asn
        305                 310                 315

ttc gtc aga aag aac gat ctg gct tac atc aac gtt gtc gac aga gat   1011
Phe Val Arg Lys Asn Asp Leu Ala Tyr Ile Asn Val Val Asp Arg Asp
    320                 325                 330

gtc gaa tac cgt ctg tac gcc gat atc tct atc gcc aaa cct gaa aag   1059
Val Glu Tyr Arg Leu Tyr Ala Asp Ile Ser Ile Ala Lys Pro Glu Lys
335                 340                 345                 350

atc atc aag ctg atc cgt acc tct aac tct aac aac tct ctg gga caa   1107
Ile Ile Lys Leu Ile Arg Thr Ser Asn Ser Asn Asn Ser Leu Gly Gln
                355                 360                 365

atc atc gtc atg gac tcc atc ggt aat aac tgt acc atg aac ttc cag   1155
Ile Ile Val Met Asp Ser Ile Gly Asn Asn Cys Thr Met Asn Phe Gln
            370                 375                 380

aac aac aac ggt gga aac atc ggt ttg ttg ggt ttc cac tcc aac aac   1203
Asn Asn Asn Gly Gly Asn Ile Gly Leu Leu Gly Phe His Ser Asn Asn
        385                 390                 395
```

```
ttg gtc gct tcc tcc tgg tac tac aac aac atc cgt aag aac acc tcc   1251
Leu Val Ala Ser Ser Trp Tyr Tyr Asn Asn Ile Arg Lys Asn Thr Ser
    400                 405                 410

tcc aac ggt tgc ttc tgg tcc ttc atc tcc aag gag cac ggt tgg cag   1299
Ser Asn Gly Cys Phe Trp Ser Phe Ile Ser Lys Glu His Gly Trp Gln
415                 420                 425                 430

gag aac taataggaat tc                                             1317
Glu Asn
```

<210> 16
<211> 432
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 16

```
Met Ser Tyr Thr Asn Asp Lys Ile Leu Ile Leu Tyr Phe Asn Lys Leu
 1               5                  10                  15
Tyr Lys Lys Ile Lys Asp Asn Ser Ile Leu Asp Met Arg Tyr Glu Asn
            20                  25                  30
Asn Lys Phe Ile Asp Ile Ser Gly Tyr Gly Ser Asn Ile Ser Ile Asn
        35                  40                  45
Gly Asp Val Tyr Ile Tyr Ser Thr Asn Arg Asn Gln Phe Gly Ile Tyr
    50                  55                  60
Ser Ser Lys Pro Ser Glu Val Asn Ile Ala Gln Asn Asn Asp Ile Ile
65                  70                  75                  80
Tyr Asn Gly Arg Tyr Gln Asn Phe Ser Ile Ser Phe Trp Val Arg Ile
                85                  90                  95
Pro Lys Tyr Phe Asn Lys Val Asn Leu Asn Asn Glu Tyr Thr Ile Ile
            100                 105                 110
Asp Cys Ile Arg Asn Asn Asn Ser Gly Trp Lys Ile Ser Leu Asn Tyr
        115                 120                 125
Asn Lys Ile Ile Trp Thr Leu Gln Asp Thr Ala Gly Asn Asn Gln Lys
    130                 135                 140
Leu Val Phe Asn Tyr Thr Gln Met Ile Ser Ile Ser Asp Tyr Ile Asn
145                 150                 155                 160
Lys Trp Ile Phe Val Thr Ile Thr Asn Asn Arg Leu Gly Asn Ser Arg
                165                 170                 175
Ile Tyr Ile Asn Gly Asn Leu Ile Asp Glu Lys Ser Ile Ser Asn Leu
            180                 185                 190
Gly Asp Ile His Val Ser Asp Asn Ile Leu Phe Lys Ile Val Gly Cys
        195                 200                 205
Asn Asp Thr Arg Tyr Val Gly Ile Arg Tyr Phe Lys Val Phe Asp Thr
    210                 215                 220
Glu Leu Gly Lys Thr Glu Ile Glu Thr Leu Tyr Ser Asp Glu Pro Asp
225                 230                 235                 240
Pro Ser Ile Leu Lys Asp Phe Trp Gly Asn Tyr Leu Leu Tyr Asn Lys
                245                 250                 255
Arg Tyr Tyr Leu Leu Asn Leu Leu Arg Thr Asp Lys Ser Ile Thr Gln
            260                 265                 270
Asn Ser Asn Phe Leu Asn Ile Asn Gln Gln Arg Gly Val Tyr Gln Lys
```

```
        275                 280                 285
Pro Asn Ile Phe Ser Asn Thr Arg Leu Tyr Thr Gly Val Glu Val Ile
    290                 295                 300
Ile Arg Lys Asn Gly Ser Thr Asp Ile Ser Asn Thr Asp Asn Phe Val
305                 310                 315                 320
Arg Lys Asn Asp Leu Ala Tyr Ile Asn Val Val Asp Arg Asp Val Glu
                325                 330                 335
Tyr Arg Leu Tyr Ala Asp Ile Ser Ile Ala Lys Pro Glu Lys Ile Ile
            340                 345                 350
Lys Leu Ile Arg Thr Ser Asn Ser Asn Asn Ser Leu Gly Gln Ile Ile
        355                 360                 365
Val Met Asp Ser Ile Gly Asn Asn Cys Thr Met Asn Phe Gln Asn Asn
    370                 375                 380
Asn Gly Gly Asn Ile Gly Leu Leu Gly Phe His Ser Asn Asn Leu Val
385                 390                 395                 400
Ala Ser Ser Trp Tyr Tyr Asn Asn Ile Arg Lys Asn Thr Ser Ser Asn
                405                 410                 415
Gly Cys Phe Trp Ser Phe Ile Ser Lys Glu His Gly Trp Gln Glu Asn
            420                 425                 430
```

<210> 17
<211> 1368
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<221> CDS
<222> (10)...(1356)

<400> 17

```
gaattcacg atg aag gac acc atc ctg atc cag gtc ttc aac aac tac atc 51
          Met Lys Asp Thr Ile Leu Ile Gln Val Phe Asn Asn Tyr Ile
           1               5                  10

tcc aac atc tcc tcc aac gcc atc ctg tcc ctg tcc tac cgt ggt ggt   99
Ser Asn Ile Ser Ser Asn Ala Ile Leu Ser Leu Ser Tyr Arg Gly Gly
 15                  20                  25                  30

cgt ctg atc gac tcc tcc ggt tac gga gcc acc atg aac gtc ggt tcc   147
Arg Leu Ile Asp Ser Ser Gly Tyr Gly Ala Thr Met Asn Val Gly Ser
                 35                  40                  45

gac gtc atc ttc aac gac atc ggt aac ggt cag ttc aag ctg aac aac   195
Asp Val Ile Phe Asn Asp Ile Gly Asn Gly Gln Phe Lys Leu Asn Asn
             50                  55                  60

tcc gag aac tcc aac atc acc gcc cac cag tcc aag ttc gtc gtc tac   243
Ser Glu Asn Ser Asn Ile Thr Ala His Gln Ser Lys Phe Val Val Tyr
         65                  70                  75

gac tcc atg ttc gac aac ttc tcc atc aac ttc tgg gtc cgt acc cca   291
Asp Ser Met Phe Asp Asn Phe Ser Ile Asn Phe Trp Val Arg Thr Pro
     80                  85                  90
```

```
aag tac aac aac aac gac atc cag acc tac ctg cag aac gag tac acc   339
Lys Tyr Asn Asn Asn Asp Ile Gln Thr Tyr Leu Gln Asn Glu Tyr Thr
 95                 100                 105                 110

atc atc tcc tgt atc aag aac gac tcc ggt tgg aag gtc tcc atc aag   387
Ile Ile Ser Cys Ile Lys Asn Asp Ser Gly Trp Lys Val Ser Ile Lys
                115                 120                 125

gga aac cgt atc atc tgg acc ctg atc gac gtc aac gcc aag tcc aag   435
Gly Asn Arg Ile Ile Trp Thr Leu Ile Asp Val Asn Ala Lys Ser Lys
            130                 135                 140

tcc atc ttc ttc gag tac tcc atc aag gac aac atc tcc gac tac atc   483
Ser Ile Phe Phe Glu Tyr Ser Ile Lys Asp Asn Ile Ser Asp Tyr Ile
        145                 150                 155

aac aag tgg ttc tcc atc acc atc acc aac gac cgt ctg ggt aac gcc   531
Asn Lys Trp Phe Ser Ile Thr Ile Thr Asn Asp Arg Leu Gly Asn Ala
    160                 165                 170

aac atc tac atc aac ggt tcc ctg aag aag tcc gag aag atc ctg aac   579
Asn Ile Tyr Ile Asn Gly Ser Leu Lys Lys Ser Glu Lys Ile Leu Asn
175                 180                 185                 190

ctg gac cgt atc aac tcc tcc aac gac atc gac ttc aag ctg atc aac   627
Leu Asp Arg Ile Asn Ser Ser Asn Asp Ile Asp Phe Lys Leu Ile Asn
                195                 200                 205

tgt acc gac acc acc aag ttc gtc tgg atc aag gac ttc aac atc ttc   675
Cys Thr Asp Thr Thr Lys Phe Val Trp Ile Lys Asp Phe Asn Ile Phe
            210                 215                 220

ggt cgt gag ctg aac gcc acc gag gtc tcc tcc ctg tac tgg atc cag   723
Gly Arg Glu Leu Asn Ala Thr Glu Val Ser Ser Leu Tyr Trp Ile Gln
        225                 230                 235

tcc tcc acc aac acc ctg aag gac ttc tgg gga aac cca ctg cgt tac   771
Ser Ser Thr Asn Thr Leu Lys Asp Phe Trp Gly Asn Pro Leu Arg Tyr
    240                 245                 250

gac acc cag tac tac ctg ttc aac cag ggt atg cag aac atc tac atc   819
Asp Thr Gln Tyr Tyr Leu Phe Asn Gln Gly Met Gln Asn Ile Tyr Ile
255                 260                 265                 270

aag tac ttc tcc aag gcc tcc atg ggt gag acc gcc cct cgt acc aac   867
Lys Tyr Phe Ser Lys Ala Ser Met Gly Glu Thr Ala Pro Arg Thr Asn
                275                 280                 285

ttc aac aac gcc gcc atc aac tac cag aac ctg tac ctg ggt ctg cgt   915
Phe Asn Asn Ala Ala Ile Asn Tyr Gln Asn Leu Tyr Leu Gly Leu Arg
            290                 295                 300

ttc atc atc aag aag gcc tcc aac tcc cgt aac atc aac aac gac aac   963
Phe Ile Ile Lys Lys Ala Ser Asn Ser Arg Asn Ile Asn Asn Asp Asn
        305                 310                 315

atc gtc cgt gag ggt gac tac atc tac ctg aac atc gac aac atc tcc   1011
```

```
Ile Val Arg Glu Gly Asp Tyr Ile Tyr Leu Asn Ile Asp Asn Ile Ser
    320                 325                 330

gac gag tcc tac cgt gtc tac gtc ctg gtc aac tcc aag gag atc cag   1059
Asp Glu Ser Tyr Arg Val Tyr Val Leu Val Asn Ser Lys Glu Ile Gln
335                 340                 345                 350

acc cag ctg ttc ctg gcc cca atc aac gac gac cct acc ttc tac gac   1107
Thr Gln Leu Phe Leu Ala Pro Ile Asn Asp Asp Pro Thr Phe Tyr Asp
                355                 360                 365

gtc ctg cag atc aag aag tac tac gag aag acc acc tac aac tgt cag   1155
Val Leu Gln Ile Lys Lys Tyr Tyr Glu Lys Thr Thr Tyr Asn Cys Gln
            370                 375                 380

atc ctg tgc gag aag gac acc aag acc ttc gga ctg ttc ggt atc ggt   1203
Ile Leu Cys Glu Lys Asp Thr Lys Thr Phe Gly Leu Phe Gly Ile Gly
        385                 390                 395

aag ttc gtc aag gac tac ggt tac gtc tgg gac acc tac gac aac tac   1251
Lys Phe Val Lys Asp Tyr Gly Tyr Val Trp Asp Thr Tyr Asp Asn Tyr
    400                 405                 410

ttc tgt atc tcc cag tgg tac ctg cgt cgt atc tcc gag aac atc aac   1299
Phe Cys Ile Ser Gln Trp Tyr Leu Arg Arg Ile Ser Glu Asn Ile Asn
415                 420                 425                 430

aag ctg cgt ctg gga tgt aac tgg cag ttc atc cca gtc gac gag ggt   1347
Lys Leu Arg Leu Gly Cys Asn Trp Gln Phe Ile Pro Val Asp Glu Gly
                435                 440                 445

tgg acc gag taataggaat tc                                        1368
Trp Thr Glu
```

<210> 18
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 18

```
Met Lys Asp Thr Ile Leu Ile Gln Val Phe Asn Asn Tyr Ile Ser Asn
 1               5                  10                  15
Ile Ser Ser Asn Ala Ile Leu Ser Leu Ser Tyr Arg Gly Gly Arg Leu
            20                  25                  30
Ile Asp Ser Ser Gly Tyr Gly Ala Thr Met Asn Val Gly Ser Asp Val
        35                  40                  45
Ile Phe Asn Asp Ile Gly Asn Gly Gln Phe Lys Leu Asn Asn Ser Glu
    50                  55                  60
Asn Ser Asn Ile Thr Ala His Gln Ser Lys Phe Val Val Tyr Asp Ser
65                  70                  75                  80
Met Phe Asp Asn Phe Ser Ile Asn Phe Trp Val Arg Thr Pro Lys Tyr
                85                  90                  95
```

```
Asn Asn Asn Asp Ile Gln Thr Tyr Leu Gln Asn Glu Tyr Thr Ile Ile
            100                 105                 110
Ser Cys Ile Lys Asn Asp Ser Gly Trp Lys Val Ser Ile Lys Gly Asn
        115                 120                 125
Arg Ile Ile Trp Thr Leu Ile Asp Val Asn Ala Lys Ser Lys Ser Ile
    130                 135                 140
Phe Phe Glu Tyr Ser Ile Lys Asp Asn Ile Ser Asp Tyr Ile Asn Lys
145                 150                 155                 160
Trp Phe Ser Ile Thr Ile Thr Asn Asp Arg Leu Gly Asn Ala Asn Ile
                165                 170                 175
Tyr Ile Asn Gly Ser Leu Lys Lys Ser Glu Lys Ile Leu Asn Leu Asp
            180                 185                 190
Arg Ile Asn Ser Ser Asn Asp Ile Asp Phe Lys Leu Ile Asn Cys Thr
        195                 200                 205
Asp Thr Thr Lys Phe Val Trp Ile Lys Asp Phe Asn Ile Phe Gly Arg
    210                 215                 220
Glu Leu Asn Ala Thr Glu Val Ser Ser Leu Tyr Trp Ile Gln Ser Ser
225                 230                 235                 240
Thr Asn Thr Leu Lys Asp Phe Trp Gly Asn Pro Leu Arg Tyr Asp Thr
                245                 250                 255
Gln Tyr Tyr Leu Phe Asn Gln Gly Met Gln Asn Ile Tyr Ile Lys Tyr
            260                 265                 270
Phe Ser Lys Ala Ser Met Gly Glu Thr Ala Pro Arg Thr Asn Phe Asn
        275                 280                 285
Asn Ala Ala Ile Asn Tyr Gln Asn Leu Tyr Leu Gly Leu Arg Phe Ile
    290                 295                 300
Ile Lys Lys Ala Ser Asn Ser Arg Asn Ile Asn Asn Asp Asn Ile Val
305                 310                 315                 320
Arg Glu Gly Asp Tyr Ile Tyr Leu Asn Ile Asp Asn Ile Ser Asp Glu
                325                 330                 335
Ser Tyr Arg Val Tyr Val Leu Val Asn Ser Lys Glu Ile Gln Thr Gln
            340                 345                 350
Leu Phe Leu Ala Pro Ile Asn Asp Asp Pro Thr Phe Tyr Asp Val Leu
        355                 360                 365
Gln Ile Lys Lys Tyr Tyr Glu Lys Thr Thr Tyr Asn Cys Gln Ile Leu
    370                 375                 380
Cys Glu Lys Asp Thr Lys Thr Phe Gly Leu Phe Gly Ile Gly Lys Phe
385                 390                 395                 400
Val Lys Asp Tyr Gly Tyr Val Trp Asp Thr Tyr Asp Asn Tyr Phe Cys
                405                 410                 415
Ile Ser Gln Trp Tyr Leu Arg Arg Ile Ser Glu Asn Ile Asn Lys Leu
            420                 425                 430
Arg Leu Gly Cys Asn Trp Gln Phe Ile Pro Val Asp Glu Gly Trp Thr
        435                 440                 445
Glu
```

<210> 19
<211> 1242
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<221> CDS

<222> (1)...(1239)

<400> 19

```
atg gct ctg aac gac ctg tgc atc aaa gtt aac aac tgg gac ctg ttc   48
Met Ala Leu Asn Asp Leu Cys Ile Lys Val Asn Asn Trp Asp Leu Phe
 1               5                  10                  15

ttc tcc ccg tct gaa gac aac ttc act aac gac ctg aac aaa ggc gaa   96
Phe Ser Pro Ser Glu Asp Asn Phe Thr Asn Asp Leu Asn Lys Gly Glu
            20                  25                  30

gaa atc acc tcc gac act aac atc gaa gct gct gaa gaa aac atc tct   144
Glu Ile Thr Ser Asp Thr Asn Ile Glu Ala Ala Glu Glu Asn Ile Ser
        35                  40                  45

ctg gac ctg atc cag cag tac tac ctg act ttc aac ttc gac aac gaa   192
Leu Asp Leu Ile Gln Gln Tyr Tyr Leu Thr Phe Asn Phe Asp Asn Glu
    50                  55                  60

ccg gaa aac atc tcc atc gaa aac ctg tct tcc gac atc atc ggt cag   240
Pro Glu Asn Ile Ser Ile Glu Asn Leu Ser Ser Asp Ile Ile Gly Gln
65                  70                  75                  80

ctg gaa ctg atg ccg aac atc gaa cgc ttc ccg aac ggc aag aaa tac   288
Leu Glu Leu Met Pro Asn Ile Glu Arg Phe Pro Asn Gly Lys Lys Tyr
                85                  90                  95

gaa ctg gac aaa tac acc atg ttc cac tac ctg cgt gct cag gaa ttc   336
Glu Leu Asp Lys Tyr Thr Met Phe His Tyr Leu Arg Ala Gln Glu Phe
            100                 105                 110

gaa cac ggt aaa tct cgt atc gct ctg act aac tcc gtt aac gaa gct   384
Glu His Gly Lys Ser Arg Ile Ala Leu Thr Asn Ser Val Asn Glu Ala
        115                 120                 125

ctg ctg aac ccg tct cgc gtt tac acc ttc ttc tct tcc gac tac gtt   432
Leu Leu Asn Pro Ser Arg Val Tyr Thr Phe Phe Ser Ser Asp Tyr Val
    130                 135                 140

aag aaa gtt aac aaa gct act gaa gct gct atg ttc ctg ggt tgg gtt   480
Lys Lys Val Asn Lys Ala Thr Glu Ala Ala Met Phe Leu Gly Trp Val
145                 150                 155                 160

gaa cag ctg gtt tac gac ttc acc gac gaa act tct gaa gtt tcc acc   528
Glu Gln Leu Val Tyr Asp Phe Thr Asp Glu Thr Ser Glu Val Ser Thr
                165                 170                 175

act gac aaa atc gct gac atc act atc atc atc ccg tac atc ggc ccg   576
Thr Asp Lys Ile Ala Asp Ile Thr Ile Ile Ile Pro Tyr Ile Gly Pro
            180                 185                 190

gct ctg aac atc ggt aac atg ctg tac aaa gac gac ttc gtt ggt gct   624
Ala Leu Asn Ile Gly Asn Met Leu Tyr Lys Asp Asp Phe Val Gly Ala
        195                 200                 205

ctg atc ttc tct ggc gct gtt atc ctg ctg gaa ttc atc ccg gaa atc   672
Leu Ile Phe Ser Gly Ala Val Ile Leu Leu Glu Phe Ile Pro Glu Ile
```

```
    210                 215                 220

gct atc ccg gtt ctg ggt acc ttc gct ctg gtt tcc tac atc gct aac   720
Ala Ile Pro Val Leu Gly Thr Phe Ala Leu Val Ser Tyr Ile Ala Asn
225                 230                 235                 240

aaa gtt ctg act gtt cag acc atc gac aac gct ctg tct aaa cgt aac   768
Lys Val Leu Thr Val Gln Thr Ile Asp Asn Ala Leu Ser Lys Arg Asn
                245                 250                 255

gaa aaa tgg gac gaa gtt tac aaa tac atc gtt act aac tgg ctg gct   816
Glu Lys Trp Asp Glu Val Tyr Lys Tyr Ile Val Thr Asn Trp Leu Ala
            260                 265                 270

aaa gtt aac act cag atc gac ctg atc cgt aag aag atg aaa gaa gct   864
Lys Val Asn Thr Gln Ile Asp Leu Ile Arg Lys Lys Met Lys Glu Ala
        275                 280                 285

ctg gaa aac cag gct gaa gct act aaa gct atc atc aac tac cag tac   912
Leu Glu Asn Gln Ala Glu Ala Thr Lys Ala Ile Ile Asn Tyr Gln Tyr
    290                 295                 300

aac cag tac acc gaa gaa gaa aag aac aac atc aac ttc aac atc gat   960
Asn Gln Tyr Thr Glu Glu Glu Lys Asn Asn Ile Asn Phe Asn Ile Asp
305                 310                 315                 320

gac ctg tcc tct aaa ctg aac gaa tcc atc aac aaa gct atg atc aac  1008
Asp Leu Ser Ser Lys Leu Asn Glu Ser Ile Asn Lys Ala Met Ile Asn
                325                 330                 335

atc aac aaa ttc ctg aac cag tgc tct gtt tcc tac ctg atg aac tct  1056
Ile Asn Lys Phe Leu Asn Gln Cys Ser Val Ser Tyr Leu Met Asn Ser
            340                 345                 350

atg atc ccg tac ggc gtt aaa cgc ctg gaa gac ttc gac gct tcc ctg  1104
Met Ile Pro Tyr Gly Val Lys Arg Leu Glu Asp Phe Asp Ala Ser Leu
        355                 360                 365

aaa gac gct ctg ctg aaa tac atc cgt gac aac tac ggt act ctg atc  1152
Lys Asp Ala Leu Leu Lys Tyr Ile Arg Asp Asn Tyr Gly Thr Leu Ile
    370                 375                 380

ggc cag gtt gac cgt ctg aaa gac aag gtt aac aac acc ctg tct act  1200
Gly Gln Val Asp Arg Leu Lys Asp Lys Val Asn Asn Thr Leu Ser Thr
385                 390                 395                 400

gac atc ccg ttc cag ctg tcc aaa tac gtt gac aac cag taa          1242
Asp Ile Pro Phe Gln Leu Ser Lys Tyr Val Asp Asn Gln
                405                 410
```

<210> 20
<211> 413
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 20

```
Met Ala Leu Asn Asp Leu Cys Ile Lys Val Asn Asn Trp Asp Leu Phe
 1               5                  10                  15
Phe Ser Pro Ser Glu Asp Asn Phe Thr Asn Asp Leu Asn Lys Gly Glu
            20                  25                  30
Glu Ile Thr Ser Asp Thr Asn Ile Glu Ala Ala Glu Glu Asn Ile Ser
        35                  40                  45
Leu Asp Leu Ile Gln Gln Tyr Tyr Leu Thr Phe Asn Phe Asp Asn Glu
    50                  55                  60
Pro Glu Asn Ile Ser Ile Glu Asn Leu Ser Ser Asp Ile Ile Gly Gln
65                  70                  75                  80
Leu Glu Leu Met Pro Asn Ile Glu Arg Phe Pro Asn Gly Lys Lys Tyr
                85                  90                  95
Glu Leu Asp Lys Tyr Thr Met Phe His Tyr Leu Arg Ala Gln Glu Phe
            100                 105                 110
Glu His Gly Lys Ser Arg Ile Ala Leu Thr Asn Ser Val Asn Glu Ala
        115                 120                 125
Leu Leu Asn Pro Ser Arg Val Tyr Thr Phe Phe Ser Ser Asp Tyr Val
    130                 135                 140
Lys Lys Val Asn Lys Ala Thr Glu Ala Ala Met Phe Leu Gly Trp Val
145                 150                 155                 160
Glu Gln Leu Val Tyr Asp Phe Thr Asp Glu Thr Ser Glu Val Ser Thr
                165                 170                 175
Thr Asp Lys Ile Ala Asp Ile Thr Ile Ile Ile Pro Tyr Ile Gly Pro
            180                 185                 190
Ala Leu Asn Ile Gly Asn Met Leu Tyr Lys Asp Asp Phe Val Gly Ala
        195                 200                 205
Leu Ile Phe Ser Gly Ala Val Ile Leu Leu Glu Phe Ile Pro Glu Ile
    210                 215                 220
Ala Ile Pro Val Leu Gly Thr Phe Ala Leu Val Ser Tyr Ile Ala Asn
225                 230                 235                 240
Lys Val Leu Thr Val Gln Thr Ile Asp Asn Ala Leu Ser Lys Arg Asn
                245                 250                 255
Glu Lys Trp Asp Glu Val Tyr Lys Tyr Ile Val Thr Asn Trp Leu Ala
            260                 265                 270
Lys Val Asn Thr Gln Ile Asp Leu Ile Arg Lys Lys Met Lys Glu Ala
        275                 280                 285
Leu Glu Asn Gln Ala Glu Ala Thr Lys Ala Ile Ile Asn Tyr Gln Tyr
    290                 295                 300
Asn Gln Tyr Thr Glu Glu Glu Lys Asn Asn Ile Asn Phe Asn Ile Asp
305                 310                 315                 320
Asp Leu Ser Ser Lys Leu Asn Glu Ser Ile Asn Lys Ala Met Ile Asn
                325                 330                 335
Ile Asn Lys Phe Leu Asn Gln Cys Ser Val Ser Tyr Leu Met Asn Ser
            340                 345                 350
Met Ile Pro Tyr Gly Val Lys Arg Leu Glu Asp Phe Asp Ala Ser Leu
        355                 360                 365
Lys Asp Ala Leu Leu Lys Tyr Ile Arg Asp Asn Tyr Gly Thr Leu Ile
    370                 375                 380
Gly Gln Val Asp Arg Leu Lys Asp Lys Val Asn Asn Thr Leu Ser Thr
385                 390                 395                 400
Asp Ile Pro Phe Gln Leu Ser Lys Tyr Val Asp Asn Gln
                405                 410
```

<210> 21
<211> 1242
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<221> CDS
<222> (1)...(1239)

<400> 21
```
atg gct cca gga atc tgt atc gac gtc gac aac gag gac ttg ttc ttc   48
Met Ala Pro Gly Ile Cys Ile Asp Val Asp Asn Glu Asp Leu Phe Phe
 1               5                  10                  15

atc gct gac aag aac tcc ttc tcc gac gac ttg tcc aag aac gag aga   96
Ile Ala Asp Lys Asn Ser Phe Ser Asp Asp Leu Ser Lys Asn Glu Arg
            20                  25                  30

atc gag tac aac acc cag tcc aac tac atc gag aac gac ttc cca atc   144
Ile Glu Tyr Asn Thr Gln Ser Asn Tyr Ile Glu Asn Asp Phe Pro Ile
        35                  40                  45

aac gag ttg atc ttg gac acc gac ttg atc tcc aag atc gag ttg cca   192
Asn Glu Leu Ile Leu Asp Thr Asp Leu Ile Ser Lys Ile Glu Leu Pro
    50                  55                  60

tcc gag aac acc gag tcc ttg act gac ttc aac gtc gac gtc cca gtc   240
Ser Glu Asn Thr Glu Ser Leu Thr Asp Phe Asn Val Asp Val Pro Val
65                  70                  75                  80

tac gag aag caa cca gct atc aag aag att ttc acc gac gag aac acc   288
Tyr Glu Lys Gln Pro Ala Ile Lys Lys Ile Phe Thr Asp Glu Asn Thr
                85                  90                  95

atc ttc caa tac ctg tac tct cag acc ttc cct ttg gac atc aga gac   336
Ile Phe Gln Tyr Leu Tyr Ser Gln Thr Phe Pro Leu Asp Ile Arg Asp
            100                 105                 110

atc tcc ttg acc tct tcc ttc gac gac gcc ctg ctg ttc tcc aac aag   384
Ile Ser Leu Thr Ser Ser Phe Asp Asp Ala Leu Leu Phe Ser Asn Lys
        115                 120                 125

gtc tac tcc ttc ttc tcc atg gac tac atc aag act gct aac aag gtc   432
Val Tyr Ser Phe Phe Ser Met Asp Tyr Ile Lys Thr Ala Asn Lys Val
    130                 135                 140

gtc gag gcc ggt ttg ttc gct ggt tgg gtc aag cag atc gtc aac gat   480
Val Glu Ala Gly Leu Phe Ala Gly Trp Val Lys Gln Ile Val Asn Asp
145                 150                 155                 160

ttc gtc atc gag gct aac aag tcc aac acc atg gac aag att gcc gac   528
Phe Val Ile Glu Ala Asn Lys Ser Asn Thr Met Asp Lys Ile Ala Asp
                165                 170                 175

atc tcc ttg att gtc cca tac atc ggt ttg gcc ttg aac gtc ggt aac   576
```

```
Ile Ser Leu Ile Val Pro Tyr Ile Gly Leu Ala Leu Asn Val Gly Asn
            180                 185                 190

gag acc gcc aag ggt aac ttc gag aac gct ttc gag atc gct ggt gcc   624
Glu Thr Ala Lys Gly Asn Phe Glu Asn Ala Phe Glu Ile Ala Gly Ala
        195                 200                 205

tcc atc ttg ttg gag ttc atc cca gag ttg ttg atc cca gtc gtc ggt   672
Ser Ile Leu Leu Glu Phe Ile Pro Glu Leu Leu Ile Pro Val Val Gly
    210                 215                 220

gcc ttc ttg ttg gag tcc tac atc gac aac aag aac aag atc atc aag   720
Ala Phe Leu Leu Glu Ser Tyr Ile Asp Asn Lys Asn Lys Ile Ile Lys
225                 230                 235                 240

acc atc gac aac gct ttg acc aag aga aac gag aag tgg tcc gac atg   768
Thr Ile Asp Asn Ala Leu Thr Lys Arg Asn Glu Lys Trp Ser Asp Met
                245                 250                 255

tac ggt ttg atc gtc gcc caa tgg ttg tcc acc gtc aac acc caa ttc   816
Tyr Gly Leu Ile Val Ala Gln Trp Leu Ser Thr Val Asn Thr Gln Phe
            260                 265                 270

tac acc atc aag gag ggt atg tac aag gcc ttg aac tac cag gcc caa   864
Tyr Thr Ile Lys Glu Gly Met Tyr Lys Ala Leu Asn Tyr Gln Ala Gln
        275                 280                 285

gct ttg gag gag atc atc aag tac aga tac aac atc tac tcc gag aag   912
Ala Leu Glu Glu Ile Ile Lys Tyr Arg Tyr Asn Ile Tyr Ser Glu Lys
    290                 295                 300

gag aag tcc aac att aac atc gac ttc aac gac atc aac tcc aag ctg   960
Glu Lys Ser Asn Ile Asn Ile Asp Phe Asn Asp Ile Asn Ser Lys Leu
305                 310                 315                 320

aac gag ggt att aac cag gcc atc gac aac atc aac aac ttc atc aac   1008
Asn Glu Gly Ile Asn Gln Ala Ile Asp Asn Ile Asn Asn Phe Ile Asn
                325                 330                 335

ggt tgt tcc gtc tcc tac ttg atg aag aag atg att cca ttg gcc gtc   1056
Gly Cys Ser Val Ser Tyr Leu Met Lys Lys Met Ile Pro Leu Ala Val
            340                 345                 350

gag aag ttg ttg gac ttc gac aac acc ctg aag aag aac ttg ttg aac   1104
Glu Lys Leu Leu Asp Phe Asp Asn Thr Leu Lys Lys Asn Leu Leu Asn
        355                 360                 365

tac atc gac gag aac aag ttg tac ttg atc ggt tcc gct gag tac gag   1152
Tyr Ile Asp Glu Asn Lys Leu Tyr Leu Ile Gly Ser Ala Glu Tyr Glu
    370                 375                 380

aag tcc aag gtc aac aag tac ttg aag acc atc atg cca ttc gac ttg   1200
Lys Ser Lys Val Asn Lys Tyr Leu Lys Thr Ile Met Pro Phe Asp Leu
385                 390                 395                 400

tcc atc tac acc aac gac acc atc ttg atc gag atg ttc taa           1242
Ser Ile Tyr Thr Asn Asp Thr Ile Leu Ile Glu Met Phe
```

405 410

<210> 22
<211> 413
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 22
Met Ala Pro Gly Ile Cys Ile Asp Val Asp Asn Glu Asp Leu Phe Phe
1 5 10 15
Ile Ala Asp Lys Asn Ser Phe Ser Asp Asp Leu Ser Lys Asn Glu Arg
20 25 30
Ile Glu Tyr Asn Thr Gln Ser Asn Tyr Ile Glu Asn Asp Phe Pro Ile
35 40 45
Asn Glu Leu Ile Leu Asp Thr Asp Leu Ile Ser Lys Ile Glu Leu Pro
50 55 60
Ser Glu Asn Thr Glu Ser Leu Thr Asp Phe Asn Val Asp Val Pro Val
65 70 75 80
Tyr Glu Lys Gln Pro Ala Ile Lys Lys Ile Phe Thr Asp Glu Asn Thr
85 90 95
Ile Phe Gln Tyr Leu Tyr Ser Gln Thr Phe Pro Leu Asp Ile Arg Asp
100 105 110
Ile Ser Leu Thr Ser Ser Phe Asp Asp Ala Leu Leu Phe Ser Asn Lys
115 120 125
Val Tyr Ser Phe Phe Ser Met Asp Tyr Ile Lys Thr Ala Asn Lys Val
130 135 140
Val Glu Ala Gly Leu Phe Ala Gly Trp Val Lys Gln Ile Val Asn Asp
145 150 155 160
Phe Val Ile Glu Ala Asn Lys Ser Asn Thr Met Asp Lys Ile Ala Asp
165 170 175
Ile Ser Leu Ile Val Pro Tyr Ile Gly Leu Ala Leu Asn Val Gly Asn
180 185 190
Glu Thr Ala Lys Gly Asn Phe Glu Asn Ala Phe Glu Ile Ala Gly Ala
195 200 205
Ser Ile Leu Leu Glu Phe Ile Pro Glu Leu Leu Ile Pro Val Val Gly
210 215 220
Ala Phe Leu Leu Glu Ser Tyr Ile Asp Asn Lys Asn Lys Ile Ile Lys
225 230 235 240
Thr Ile Asp Asn Ala Leu Thr Lys Arg Asn Glu Lys Trp Ser Asp Met
245 250 255
Tyr Gly Leu Ile Val Ala Gln Trp Leu Ser Thr Val Asn Thr Gln Phe
260 265 270
Tyr Thr Ile Lys Glu Gly Met Tyr Lys Ala Leu Asn Tyr Gln Ala Gln
275 280 285
Ala Leu Glu Glu Ile Ile Lys Tyr Arg Tyr Asn Ile Tyr Ser Glu Lys
290 295 300
Glu Lys Ser Asn Ile Asn Ile Asp Phe Asn Asp Ile Asn Ser Lys Leu
305 310 315 320
Asn Glu Gly Ile Asn Gln Ala Ile Asp Asn Ile Asn Asn Phe Ile Asn
325 330 335
Gly Cys Ser Val Ser Tyr Leu Met Lys Lys Met Ile Pro Leu Ala Val
340 345 350
Glu Lys Leu Leu Asp Phe Asp Asn Thr Leu Lys Lys Asn Leu Leu Asn

```
        355                 360                 365
Tyr Ile Asp Glu Asn Lys Leu Tyr Leu Ile Gly Ser Ala Glu Tyr Glu
    370                 375                 380
Lys Ser Lys Val Asn Lys Tyr Leu Lys Thr Ile Met Pro Phe Asp Leu
385                 390                 395                 400
Ser Ile Tyr Thr Asn Asp Thr Ile Leu Ile Glu Met Phe
                405                 410
```

<210> 23
<211> 1200
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<221> CDS
<222> (1)...(1197)

<400> 23

```
atg tcc ctg tac aac aag acc ctt gac tgt aga gag ctg ctg gtg aag   48
Met Ser Leu Tyr Asn Lys Thr Leu Asp Cys Arg Glu Leu Leu Val Lys
 1               5                  10                  15

aac act gac ctg cca ttc atc ggt gac atc agt gac gtg aag act gac   96
Asn Thr Asp Leu Pro Phe Ile Gly Asp Ile Ser Asp Val Lys Thr Asp
            20                  25                  30

atc ttc ctg cgt aag gac atc aac gag gag act gag gtg atc tac tac   144
Ile Phe Leu Arg Lys Asp Ile Asn Glu Glu Thr Glu Val Ile Tyr Tyr
        35                  40                  45

cca gac aac gtg tca gta gac caa gtg atc ctc agt aag aac acc tcc   192
Pro Asp Asn Val Ser Val Asp Gln Val Ile Leu Ser Lys Asn Thr Ser
    50                  55                  60

gag cat gga caa cta gac ctg ctc tac cct agt atc gac agt gag agt   240
Glu His Gly Gln Leu Asp Leu Leu Tyr Pro Ser Ile Asp Ser Glu Ser
65                  70                  75                  80

gag atc ctg cca ggg gag aat caa gtc ttc tac gac aac cgt acc cag   288
Glu Ile Leu Pro Gly Glu Asn Gln Val Phe Tyr Asp Asn Arg Thr Gln
                85                  90                  95

aac gtg gac tac ctg aac tcc tac tac tac cta gag tct cag aag ctg   336
Asn Val Asp Tyr Leu Asn Ser Tyr Tyr Tyr Leu Glu Ser Gln Lys Leu
            100                 105                 110

agt gac aac gtg gag gac ttc act ttc acg cgt tca atc gag gag gct   384
Ser Asp Asn Val Glu Asp Phe Thr Phe Thr Arg Ser Ile Glu Glu Ala
        115                 120                 125

ctg gac aac agt gca aag gtg tac act tac ttc cct acc ctg gct aac   432
Leu Asp Asn Ser Ala Lys Val Tyr Thr Tyr Phe Pro Thr Leu Ala Asn
    130                 135                 140
```

```
aag gtg aat gcc ggt gtg caa ggt ggt ctg ttc ctg atg tgg gca aac   480
Lys Val Asn Ala Gly Val Gln Gly Gly Leu Phe Leu Met Trp Ala Asn
145                 150                 155                 160

gac gtg gtt gag gac ttc act acc aac atc ctg cgt aag gac aca ctg   528
Asp Val Val Glu Asp Phe Thr Thr Asn Ile Leu Arg Lys Asp Thr Leu
                165                 170                 175

gac aag atc tca gat gtg tca gct atc atc ccc tac atc gga ccc gca   576
Asp Lys Ile Ser Asp Val Ser Ala Ile Ile Pro Tyr Ile Gly Pro Ala
            180                 185                 190

ctg aac atc tcc aac tct gtg cgt cgt gga aac ttc act gag gca ttc   624
Leu Asn Ile Ser Asn Ser Val Arg Arg Gly Asn Phe Thr Glu Ala Phe
        195                 200                 205

gca gtc act ggt gtc acc atc ctg ctg gag gca ttc cct gag ttc aca   672
Ala Val Thr Gly Val Thr Ile Leu Leu Glu Ala Phe Pro Glu Phe Thr
    210                 215                 220

atc cct gct ctg ggt gca ttc gtg atc tac agt aag gtc cag gag cga   720
Ile Pro Ala Leu Gly Ala Phe Val Ile Tyr Ser Lys Val Gln Glu Arg
225                 230                 235                 240

aac gag atc atc aag acc atc gac aac tgt ctg gag cag agg atc aag   768
Asn Glu Ile Ile Lys Thr Ile Asp Asn Cys Leu Glu Gln Arg Ile Lys
                245                 250                 255

aga tgg aag gac tcc tac gag tgg atg atg gga acg tgg ttg tcc agg   816
Arg Trp Lys Asp Ser Tyr Glu Trp Met Met Gly Thr Trp Leu Ser Arg
            260                 265                 270

atc atc acc cag ttc aac aac atc tcc tac cag atg tac gac tcc ctg   864
Ile Ile Thr Gln Phe Asn Asn Ile Ser Tyr Gln Met Tyr Asp Ser Leu
        275                 280                 285

aac tac cag gca ggt gca atc aag gct aag atc gac ctg gag tac aag   912
Asn Tyr Gln Ala Gly Ala Ile Lys Ala Lys Ile Asp Leu Glu Tyr Lys
    290                 295                 300

aag tac tcc gga agc gac aag gag aac atc aag agc cag gtt gag aac   960
Lys Tyr Ser Gly Ser Asp Lys Glu Asn Ile Lys Ser Gln Val Glu Asn
305                 310                 315                 320

ctg aag aac agt ctg gac gtc aag atc tcg gag gca atg aac aac atc   1008
Leu Lys Asn Ser Leu Asp Val Lys Ile Ser Glu Ala Met Asn Asn Ile
                325                 330                 335

aac aag ttc atc cga gag tgc tcc gtc acc tac ctg ttc aag aac atg   1056
Asn Lys Phe Ile Arg Glu Cys Ser Val Thr Tyr Leu Phe Lys Asn Met
            340                 345                 350

ctg cct aag gtc atc gac gag ctg aac gag ttc gac cga aac acc aag   1104
Leu Pro Lys Val Ile Asp Glu Leu Asn Glu Phe Asp Arg Asn Thr Lys
        355                 360                 365

gca aag ctg atc aac ctg atc gac tcc cat aac atc atc ctg gtc ggt   1152
```

```
Ala Lys Leu Ile Asn Leu Ile Asp Ser His Asn Ile Ile Leu Val Gly
    370                 375                 380

gag gtc gac aag ctg aag gca aag gta aac aac agc ttc cag aac       1197
Glu Val Asp Lys Leu Lys Ala Lys Val Asn Asn Ser Phe Gln Asn
385                 390                 395

taa                                                               1200

<210> 24
<211> 399
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 24
Met Ser Leu Tyr Asn Lys Thr Leu Asp Cys Arg Glu Leu Leu Val Lys
 1               5                  10                  15
Asn Thr Asp Leu Pro Phe Ile Gly Asp Ile Ser Asp Val Lys Thr Asp
            20                  25                  30
Ile Phe Leu Arg Lys Asp Ile Asn Glu Glu Thr Glu Val Ile Tyr Tyr
        35                  40                  45
Pro Asp Asn Val Ser Val Asp Gln Val Ile Leu Ser Lys Asn Thr Ser
    50                  55                  60
Glu His Gly Gln Leu Asp Leu Leu Tyr Pro Ser Ile Asp Ser Glu Ser
65                  70                  75                  80
Glu Ile Leu Pro Gly Glu Asn Gln Val Phe Tyr Asp Asn Arg Thr Gln
                85                  90                  95
Asn Val Asp Tyr Leu Asn Ser Tyr Tyr Tyr Leu Glu Ser Gln Lys Leu
            100                 105                 110
Ser Asp Asn Val Glu Asp Phe Thr Phe Thr Arg Ser Ile Glu Glu Ala
        115                 120                 125
Leu Asp Asn Ser Ala Lys Val Tyr Thr Tyr Phe Pro Thr Leu Ala Asn
    130                 135                 140
Lys Val Asn Ala Gly Val Gln Gly Gly Leu Phe Leu Met Trp Ala Asn
145                 150                 155                 160
Asp Val Val Glu Asp Phe Thr Thr Asn Ile Leu Arg Lys Asp Thr Leu
                165                 170                 175
Asp Lys Ile Ser Asp Val Ser Ala Ile Ile Pro Tyr Ile Gly Pro Ala
            180                 185                 190
Leu Asn Ile Ser Asn Ser Val Arg Arg Gly Asn Phe Thr Glu Ala Phe
        195                 200                 205
Ala Val Thr Gly Val Thr Ile Leu Leu Glu Ala Phe Pro Glu Phe Thr
    210                 215                 220
Ile Pro Ala Leu Gly Ala Phe Val Ile Tyr Ser Lys Val Gln Glu Arg
225                 230                 235                 240
Asn Glu Ile Ile Lys Thr Ile Asp Asn Cys Leu Glu Gln Arg Ile Lys
                245                 250                 255
Arg Trp Lys Asp Ser Tyr Glu Trp Met Met Gly Thr Trp Leu Ser Arg
            260                 265                 270
Ile Ile Thr Gln Phe Asn Asn Ile Ser Tyr Gln Met Tyr Asp Ser Leu
        275                 280                 285
Asn Tyr Gln Ala Gly Ala Ile Lys Ala Lys Ile Asp Leu Glu Tyr Lys
    290                 295                 300
Lys Tyr Ser Gly Ser Asp Lys Glu Asn Ile Lys Ser Gln Val Glu Asn
```

```
305                 310                 315                 320
Leu Lys Asn Ser Leu Asp Val Lys Ile Ser Glu Ala Met Asn Asn Ile
                325                 330                 335
Asn Lys Phe Ile Arg Glu Cys Ser Val Thr Tyr Leu Phe Lys Asn Met
            340                 345                 350
Leu Pro Lys Val Ile Asp Glu Leu Asn Glu Phe Asp Arg Asn Thr Lys
        355                 360                 365
Ala Lys Leu Ile Asn Leu Ile Asp Ser His Asn Ile Ile Leu Val Gly
    370                 375                 380
Glu Val Asp Lys Leu Lys Ala Lys Val Asn Asn Ser Phe Gln Asn
385                 390                 395
```

<210> 25
<211> 1161
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<221> CDS
<222> (1)...(1158)

<400> 25

```
atg gcc aac tcc cgt gac gac tcc acc tgc atc aag gtc aag aac aac   48
Met Ala Asn Ser Arg Asp Asp Ser Thr Cys Ile Lys Val Lys Asn Asn
 1               5                  10                  15

aga ctg cca tac gtt gcc gac aag gac tcc atc tcc cag gag atc ttc   96
Arg Leu Pro Tyr Val Ala Asp Lys Asp Ser Ile Ser Gln Glu Ile Phe
            20                  25                  30

gag aac aag atc atc acc gac gag acc aac gtt caa aac tac tcc gac   144
Glu Asn Lys Ile Ile Thr Asp Glu Thr Asn Val Gln Asn Tyr Ser Asp
        35                  40                  45

aag ttc tct ttg gac gag tcc atc ctg gac ggt cag gtc cca atc aac   192
Lys Phe Ser Leu Asp Glu Ser Ile Leu Asp Gly Gln Val Pro Ile Asn
    50                  55                  60

cca gag atc gtc gac cca ctg ttg cca aac gtc aac atg gag cca ttg   240
Pro Glu Ile Val Asp Pro Leu Leu Pro Asn Val Asn Met Glu Pro Leu
65                  70                  75                  80

aac ttg cca ggt gag gag atc gtc ttc tac gac gac atc acc aag tac   288
Asn Leu Pro Gly Glu Glu Ile Val Phe Tyr Asp Asp Ile Thr Lys Tyr
                85                  90                  95

gtc gac tac ttg aac tcc tac tac tac ttg gag tct caa aag ttg tct   336
Val Asp Tyr Leu Asn Ser Tyr Tyr Tyr Leu Glu Ser Gln Lys Leu Ser
            100                 105                 110

aac aac gtc gag aac atc acc ttg acc acc tcc gtc gag gag gcc ttg   384
Asn Asn Val Glu Asn Ile Thr Leu Thr Thr Ser Val Glu Glu Ala Leu
        115                 120                 125
```

```
ggt tac tct aac aag atc tac acc ttc ctg cca tcc ttg gct gag aag   432
Gly Tyr Ser Asn Lys Ile Tyr Thr Phe Leu Pro Ser Leu Ala Glu Lys
    130                 135                 140

gtt aac aag ggt gtt caa gct ggt ttg ttc ctg aac tgg gcc aac gag   480
Val Asn Lys Gly Val Gln Ala Gly Leu Phe Leu Asn Trp Ala Asn Glu
145                 150                 155                 160

gtc gtc gag gac ttc acc acc aac atc atg aag aag gac acc ctg gac   528
Val Val Glu Asp Phe Thr Thr Asn Ile Met Lys Lys Asp Thr Leu Asp
                165                 170                 175

aag atc tcc gac gtc tcc gtc atc atc cca tac atc ggt cca gcc ttg   576
Lys Ile Ser Asp Val Ser Val Ile Ile Pro Tyr Ile Gly Pro Ala Leu
            180                 185                 190

aac atc ggt aac tcc gcc ctg aga ggt aac ttc aac cag gcc ttc gcc   624
Asn Ile Gly Asn Ser Ala Leu Arg Gly Asn Phe Asn Gln Ala Phe Ala
        195                 200                 205

acc gcc ggt gtc gcc ttc ctg ctg gag ggt ttc cca gag ttc acc atc   672
Thr Ala Gly Val Ala Phe Leu Leu Glu Gly Phe Pro Glu Phe Thr Ile
    210                 215                 220

cca gcc ctg ggt gtc ttc acc ttc tac tcc tcc atc cag gag aga gag   720
Pro Ala Leu Gly Val Phe Thr Phe Tyr Ser Ser Ile Gln Glu Arg Glu
225                 230                 235                 240

aag atc atc aag acc atc gag aac tgc ttg gag cag aga gtc aag aga   768
Lys Ile Ile Lys Thr Ile Glu Asn Cys Leu Glu Gln Arg Val Lys Arg
                245                 250                 255

tgg aag gac tcc tac cag tgg atg gtt tcc aac tgg ctg tcc aga atc   816
Trp Lys Asp Ser Tyr Gln Trp Met Val Ser Asn Trp Leu Ser Arg Ile
            260                 265                 270

acc acc caa ttc aac cac atc aac tac cag atg tac gac tcc ctg tcc   864
Thr Thr Gln Phe Asn His Ile Asn Tyr Gln Met Tyr Asp Ser Leu Ser
        275                 280                 285

tac cag gcc gac gcc atc aag gcc aag atc gac ctg gag tac aag aag   912
Tyr Gln Ala Asp Ala Ile Lys Ala Lys Ile Asp Leu Glu Tyr Lys Lys
    290                 295                 300

tac tcc ggt tcc gac aag gag aac atc aag tcc cag gtc gag aac ctg   960
Tyr Ser Gly Ser Asp Lys Glu Asn Ile Lys Ser Gln Val Glu Asn Leu
305                 310                 315                 320

aag aac tcc ttg gac gtc aag atc tcc gag gcc atg aac aac atc aac   1008
Lys Asn Ser Leu Asp Val Lys Ile Ser Glu Ala Met Asn Asn Ile Asn
                325                 330                 335

aag ttc atc cgt gag tgt tcc gtc acc tac ctg ttc aag aac atg ctg   1056
Lys Phe Ile Arg Glu Cys Ser Val Thr Tyr Leu Phe Lys Asn Met Leu
            340                 345                 350

cca aag gtc atc gac gag ctg aac aag ttc gac ctg aga acc aag acc   1104
```

```
Pro Lys Val Ile Asp Glu Leu Asn Lys Phe Asp Leu Arg Thr Lys Thr
        355                 360                 365

gag ctg atc aac ctg atc gac tcc cac aac atc atc ctg gtt ggt gag   1152
Glu Leu Ile Asn Leu Ile Asp Ser His Asn Ile Ile Leu Val Gly Glu
    370                 375                 380

gtt gac taa                                                       1161
Val Asp
385
```

<210> 26
<211> 386
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 26

```
Met Ala Asn Ser Arg Asp Asp Ser Thr Cys Ile Lys Val Lys Asn Asn
 1               5                  10                  15
Arg Leu Pro Tyr Val Ala Asp Lys Asp Ser Ile Ser Gln Glu Ile Phe
            20                  25                  30
Glu Asn Lys Ile Ile Thr Asp Glu Thr Asn Val Gln Asn Tyr Ser Asp
        35                  40                  45
Lys Phe Ser Leu Asp Glu Ser Ile Leu Asp Gly Gln Val Pro Ile Asn
    50                  55                  60
Pro Glu Ile Val Asp Pro Leu Leu Pro Asn Val Asn Met Glu Pro Leu
65                  70                  75                  80
Asn Leu Pro Gly Glu Glu Ile Val Phe Tyr Asp Asp Ile Thr Lys Tyr
                85                  90                  95
Val Asp Tyr Leu Asn Ser Tyr Tyr Tyr Leu Glu Ser Gln Lys Leu Ser
            100                 105                 110
Asn Asn Val Glu Asn Ile Thr Leu Thr Thr Ser Val Glu Glu Ala Leu
        115                 120                 125
Gly Tyr Ser Asn Lys Ile Tyr Thr Phe Leu Pro Ser Leu Ala Glu Lys
    130                 135                 140
Val Asn Lys Gly Val Gln Ala Gly Leu Phe Leu Asn Trp Ala Asn Glu
145                 150                 155                 160
Val Val Glu Asp Phe Thr Thr Asn Ile Met Lys Lys Asp Thr Leu Asp
                165                 170                 175
Lys Ile Ser Asp Val Ser Val Ile Ile Pro Tyr Ile Gly Pro Ala Leu
            180                 185                 190
Asn Ile Gly Asn Ser Ala Leu Arg Gly Asn Phe Asn Gln Ala Phe Ala
        195                 200                 205
Thr Ala Gly Val Ala Phe Leu Leu Glu Gly Phe Pro Glu Phe Thr Ile
    210                 215                 220
Pro Ala Leu Gly Val Phe Thr Phe Tyr Ser Ser Ile Gln Glu Arg Glu
225                 230                 235                 240
Lys Ile Ile Lys Thr Ile Glu Asn Cys Leu Glu Gln Arg Val Lys Arg
                245                 250                 255
Trp Lys Asp Ser Tyr Gln Trp Met Val Ser Asn Trp Leu Ser Arg Ile
            260                 265                 270
Thr Thr Gln Phe Asn His Ile Asn Tyr Gln Met Tyr Asp Ser Leu Ser
        275                 280                 285
```

```
Tyr Gln Ala Asp Ala Ile Lys Ala Lys Ile Asp Leu Glu Tyr Lys Lys
    290                 295                 300
Tyr Ser Gly Ser Asp Lys Glu Asn Ile Lys Ser Gln Val Glu Asn Leu
305                 310                 315                 320
Lys Asn Ser Leu Asp Val Lys Ile Ser Glu Ala Met Asn Asn Ile Asn
                325                 330                 335
Lys Phe Ile Arg Glu Cys Ser Val Thr Tyr Leu Phe Lys Asn Met Leu
            340                 345                 350
Pro Lys Val Ile Asp Glu Leu Asn Lys Phe Asp Leu Arg Thr Lys Thr
        355                 360                 365
Glu Leu Ile Asn Leu Ile Asp Ser His Asn Ile Ile Leu Val Gly Glu
    370                 375                 380
Val Asp
385
```

<210> 27
<211> 1149
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<221> CDS
<222> (1)...(1146)

<400> 27

```
atg tcc atc tgc atc gag atc aac aac ggt gag ctg ttc ttc gtg gct   48
Met Ser Ile Cys Ile Glu Ile Asn Asn Gly Glu Leu Phe Phe Val Ala
 1               5                  10                  15

tcc gag aac agt tac aac gat gac aac atc aac act cct aag gag att   96
Ser Glu Asn Ser Tyr Asn Asp Asp Asn Ile Asn Thr Pro Lys Glu Ile
            20                  25                  30

gac gac acc gtc act tct aac aac aac tac gaa aac gac ctg gac cag   144
Asp Asp Thr Val Thr Ser Asn Asn Asn Tyr Glu Asn Asp Leu Asp Gln
        35                  40                  45

gtc atc cta aac ttc aac tcc gag tcc gcc cct ggt ctg tcc gac gag   192
Val Ile Leu Asn Phe Asn Ser Glu Ser Ala Pro Gly Leu Ser Asp Glu
    50                  55                  60

aag ctg aac ctg acc atc cag aac gac gct tac atc cca aag tac gac   240
Lys Leu Asn Leu Thr Ile Gln Asn Asp Ala Tyr Ile Pro Lys Tyr Asp
65                  70                  75                  80

tcc aac ggt aca tcc gat atc gag cag cat gac gtt aac gag ctt aac   288
Ser Asn Gly Thr Ser Asp Ile Glu Gln His Asp Val Asn Glu Leu Asn
                85                  90                  95

gtc ttc ttc tac tta gac gct cag aag gtg ccc gag ggt gag aac aac   336
Val Phe Phe Tyr Leu Asp Ala Gln Lys Val Pro Glu Gly Glu Asn Asn
            100                 105                 110

gtc aat ctc acc tct tca att gac aca gcc ttg ttg gag cag cct aag   384
```

```
Val Asn Leu Thr Ser Ser Ile Asp Thr Ala Leu Leu Glu Gln Pro Lys
        115                 120                 125

atc tac acc ttc ttc tcc tcc gag ttc atc aac aac gtc aac aag cct   432
Ile Tyr Thr Phe Phe Ser Ser Glu Phe Ile Asn Asn Val Asn Lys Pro
    130                 135                 140

gtg cag gcc gca ttg ttc gta agc tgg att cag cag gtg tta gta gac   480
Val Gln Ala Ala Leu Phe Val Ser Trp Ile Gln Gln Val Leu Val Asp
145                 150                 155                 160

ttc act act gag gct aac cag aag tcc act gtt gac aag atc gct gac   528
Phe Thr Thr Glu Ala Asn Gln Lys Ser Thr Val Asp Lys Ile Ala Asp
                165                 170                 175

atc tcc atc gtc gtc cca tac atc ggt ctg gct ctg aac atc ggc aac   576
Ile Ser Ile Val Val Pro Tyr Ile Gly Leu Ala Leu Asn Ile Gly Asn
            180                 185                 190

gag gca cag aag ggc aac ttc aag gat gcc ctt gag ttg ttg ggt gcc   624
Glu Ala Gln Lys Gly Asn Phe Lys Asp Ala Leu Glu Leu Leu Gly Ala
        195                 200                 205

ggt att ttg ttg gag ttc gaa ccc gag ctg ctg atc cct acc atc ctg   672
Gly Ile Leu Leu Glu Phe Glu Pro Glu Leu Leu Ile Pro Thr Ile Leu
    210                 215                 220

gtc ttc acg atc aag tcc ttc ctg ggt tcc tcc gac aac aag aac aag   720
Val Phe Thr Ile Lys Ser Phe Leu Gly Ser Ser Asp Asn Lys Asn Lys
225                 230                 235                 240

gtc att aag gcc atc aac aac gcc ctg aag gag cgt gac gag aag tgg   768
Val Ile Lys Ala Ile Asn Asn Ala Leu Lys Glu Arg Asp Glu Lys Trp
                245                 250                 255

aag gaa gtc tat tcc ttc atc gtc tcg aac tgg atg acc aag atc aac   816
Lys Glu Val Tyr Ser Phe Ile Val Ser Asn Trp Met Thr Lys Ile Asn
            260                 265                 270

acc cag ttc aac aag cga aag gag cag atg tac cag gct ctg cag aac   864
Thr Gln Phe Asn Lys Arg Lys Glu Gln Met Tyr Gln Ala Leu Gln Asn
        275                 280                 285

cag gtc aac gcc atc aag acc atc atc gag tcc aag tac aac tcc tac   912
Gln Val Asn Ala Ile Lys Thr Ile Ile Glu Ser Lys Tyr Asn Ser Tyr
    290                 295                 300

acc ctg gag gag aag aac gag ctt acc aac aag tac gat atc aag cag   960
Thr Leu Glu Glu Lys Asn Glu Leu Thr Asn Lys Tyr Asp Ile Lys Gln
305                 310                 315                 320

atc gag aac gag ctg aac cag aag gtc tcc atc gcc atg aac aac atc   1008
Ile Glu Asn Glu Leu Asn Gln Lys Val Ser Ile Ala Met Asn Asn Ile
                325                 330                 335

gac agg ttc ctg acc gag tcc tcc atc tcc tac ctg atg aag ctc atc   1056
Asp Arg Phe Leu Thr Glu Ser Ser Ile Ser Tyr Leu Met Lys Leu Ile
```

```
            340                 345                 350

aac gag gtc aag atc aac aag ctg cga gag tac gac gag aat gtc aag   1104
Asn Glu Val Lys Ile Asn Lys Leu Arg Glu Tyr Asp Glu Asn Val Lys
        355                 360                 365

acg tac ctg ctg aac tac atc atc cag cac gga tcc atc ctg           1146
Thr Tyr Leu Leu Asn Tyr Ile Ile Gln His Gly Ser Ile Leu
    370                 375                 380

taa                                                               1149
```

<210> 28
<211> 382
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 28

```
Met Ser Ile Cys Ile Glu Ile Asn Asn Gly Glu Leu Phe Phe Val Ala
 1               5                  10                  15
Ser Glu Asn Ser Tyr Asn Asp Asp Asn Ile Asn Thr Pro Lys Glu Ile
            20                  25                  30
Asp Asp Thr Val Thr Ser Asn Asn Asn Tyr Glu Asn Asp Leu Asp Gln
        35                  40                  45
Val Ile Leu Asn Phe Asn Ser Glu Ser Ala Pro Gly Leu Ser Asp Glu
    50                  55                  60
Lys Leu Asn Leu Thr Ile Gln Asn Asp Ala Tyr Ile Pro Lys Tyr Asp
65                  70                  75                  80
Ser Asn Gly Thr Ser Asp Ile Glu Gln His Asp Val Asn Glu Leu Asn
                85                  90                  95
Val Phe Phe Tyr Leu Asp Ala Gln Lys Val Pro Glu Gly Glu Asn Asn
            100                 105                 110
Val Asn Leu Thr Ser Ser Ile Asp Thr Ala Leu Leu Glu Gln Pro Lys
        115                 120                 125
Ile Tyr Thr Phe Phe Ser Ser Glu Phe Ile Asn Asn Val Asn Lys Pro
    130                 135                 140
Val Gln Ala Ala Leu Phe Val Ser Trp Ile Gln Gln Val Leu Val Asp
145                 150                 155                 160
Phe Thr Thr Glu Ala Asn Gln Lys Ser Thr Val Asp Lys Ile Ala Asp
                165                 170                 175
Ile Ser Ile Val Val Pro Tyr Ile Gly Leu Ala Leu Asn Ile Gly Asn
            180                 185                 190
Glu Ala Gln Lys Gly Asn Phe Lys Asp Ala Leu Glu Leu Leu Gly Ala
        195                 200                 205
Gly Ile Leu Leu Glu Phe Glu Pro Glu Leu Leu Ile Pro Thr Ile Leu
    210                 215                 220
Val Phe Thr Ile Lys Ser Phe Leu Gly Ser Ser Asp Asn Lys Asn Lys
225                 230                 235                 240
Val Ile Lys Ala Ile Asn Asn Ala Leu Lys Glu Arg Asp Glu Lys Trp
                245                 250                 255
Lys Glu Val Tyr Ser Phe Ile Val Ser Asn Trp Met Thr Lys Ile Asn
            260                 265                 270
Thr Gln Phe Asn Lys Arg Lys Glu Gln Met Tyr Gln Ala Leu Gln Asn
        275                 280                 285
```

```
Gln Val Asn Ala Ile Lys Thr Ile Ile Glu Ser Lys Tyr Asn Ser Tyr
    290                 295                 300
Thr Leu Glu Glu Lys Asn Glu Leu Thr Asn Lys Tyr Asp Ile Lys Gln
305                 310                 315                 320
Ile Glu Asn Glu Leu Asn Gln Lys Val Ser Ile Ala Met Asn Asn Ile
                325                 330                 335
Asp Arg Phe Leu Thr Glu Ser Ser Ile Ser Tyr Leu Met Lys Leu Ile
            340                 345                 350
Asn Glu Val Lys Ile Asn Lys Leu Arg Glu Tyr Asp Glu Asn Val Lys
        355                 360                 365
Thr Tyr Leu Leu Asn Tyr Ile Ile Gln His Gly Ser Ile Leu
    370                 375                 380


<210> 29
<211> 1227
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<221> CDS
<222> (1)...(1224)

<400> 29
atg gcc cca cca cgt ctg tgt att aga gtc aac aac tca gaa tta ttc   48
Met Ala Pro Pro Arg Leu Cys Ile Arg Val Asn Asn Ser Glu Leu Phe
 1               5                  10                  15

ttt gtc gct tcc gag tca agc tac aac gag aac gat att aac aca cct   96
Phe Val Ala Ser Glu Ser Ser Tyr Asn Glu Asn Asp Ile Asn Thr Pro
            20                  25                  30

aaa gag att gac gat act acc aac cta aac aac aac tac cgg aac aac   144
Lys Glu Ile Asp Asp Thr Thr Asn Leu Asn Asn Asn Tyr Arg Asn Asn
        35                  40                  45

ttg gat gag gtt att ttg gat tac aac tca cag acc atc cct caa att   192
Leu Asp Glu Val Ile Leu Asp Tyr Asn Ser Gln Thr Ile Pro Gln Ile
    50                  55                  60

tcc aac cgt acc tta aac act ctt gtc caa gac aac tcc tac gtt cca   240
Ser Asn Arg Thr Leu Asn Thr Leu Val Gln Asp Asn Ser Tyr Val Pro
65                  70                  75                  80

aga tac gat tct aac ggt acc tca gag atc gag gag tat gat gtt gtt   288
Arg Tyr Asp Ser Asn Gly Thr Ser Glu Ile Glu Glu Tyr Asp Val Val
                85                  90                  95

gac ttt aac gtc ttt ttc tat ttg cat gcc cag aag gtg cca gaa ggt   336
Asp Phe Asn Val Phe Phe Tyr Leu His Ala Gln Lys Val Pro Glu Gly
            100                 105                 110

gaa acc aac atc tca ttg act tct tcc att gat acc gcc ttg ttg gaa   384
Glu Thr Asn Ile Ser Leu Thr Ser Ser Ile Asp Thr Ala Leu Leu Glu
        115                 120                 125
```

```
gag tcc aag gat atc ttc ttt tct tcg gag ttt atc gat act atc aac   432
Glu Ser Lys Asp Ile Phe Phe Ser Ser Glu Phe Ile Asp Thr Ile Asn
    130                 135                 140

aag cct gtc aac gcc gct ctg ttc att gat tgg att agc aag gtc atc   480
Lys Pro Val Asn Ala Ala Leu Phe Ile Asp Trp Ile Ser Lys Val Ile
145                 150                 155                 160

aga gat ttt acc act gaa gct act caa aag tcc act gtt gat aag att   528
Arg Asp Phe Thr Thr Glu Ala Thr Gln Lys Ser Thr Val Asp Lys Ile
                165                 170                 175

gct gac atc tct ttg att gtc ccc tat gtc ggt ctt gct ttg aac atc   576
Ala Asp Ile Ser Leu Ile Val Pro Tyr Val Gly Leu Ala Leu Asn Ile
            180                 185                 190

att att gag gca gaa aag ggt aac ttt gag gag gct ttt gaa ttg ttg   624
Ile Ile Glu Ala Glu Lys Gly Asn Phe Glu Glu Ala Phe Glu Leu Leu
        195                 200                 205

gga gtt ggt att ttg ttg gag ttt gtt cca gaa ctt acc att cct gtc   672
Gly Val Gly Ile Leu Leu Glu Phe Val Pro Glu Leu Thr Ile Pro Val
    210                 215                 220

att tta gtt ttt acg atc aag tcc tac atc gat tca tac gag aac aag   720
Ile Leu Val Phe Thr Ile Lys Ser Tyr Ile Asp Ser Tyr Glu Asn Lys
225                 230                 235                 240

aat aaa gca att aaa gct att aac aac tcc ttg atc gaa aga gag gct   768
Asn Lys Ala Ile Lys Ala Ile Asn Asn Ser Leu Ile Glu Arg Glu Ala
                245                 250                 255

aag tgg aag gaa atc tac tca tgg att gta tca aac tgg ctt act aga   816
Lys Trp Lys Glu Ile Tyr Ser Trp Ile Val Ser Asn Trp Leu Thr Arg
            260                 265                 270

att aac act caa ttt aac aag aga aag gag caa atg tac cag gct ctg   864
Ile Asn Thr Gln Phe Asn Lys Arg Lys Glu Gln Met Tyr Gln Ala Leu
        275                 280                 285

caa aac caa gtc gat gct atc aag act gca att gaa tac aag tac aac   912
Gln Asn Gln Val Asp Ala Ile Lys Thr Ala Ile Glu Tyr Lys Tyr Asn
    290                 295                 300

aac tat act tcc gat gag aag aac aga ctt gaa tct gaa tac aat atc   960
Asn Tyr Thr Ser Asp Glu Lys Asn Arg Leu Glu Ser Glu Tyr Asn Ile
305                 310                 315                 320

aac aac att gaa gaa gag ttg aac aag aaa gtt tct ttg gct atg aag  1008
Asn Asn Ile Glu Glu Glu Leu Asn Lys Lys Val Ser Leu Ala Met Lys
                325                 330                 335

aat atc gaa aga ttt atg acc gaa tcc tct atc tct tac ttg atg aag  1056
Asn Ile Glu Arg Phe Met Thr Glu Ser Ser Ile Ser Tyr Leu Met Lys
            340                 345                 350
```

```
ttg atc aat gag gcc aag gtt ggt aag ttg aag aag tac gat aac cac   1104
Leu Ile Asn Glu Ala Lys Val Gly Lys Leu Lys Lys Tyr Asp Asn His
        355                 360                 365

gtt aag agc gat ctg ctg aac tac att ctc gac cac aga tca atc ctg   1152
Val Lys Ser Asp Leu Leu Asn Tyr Ile Leu Asp His Arg Ser Ile Leu
    370                 375                 380

gga gag cag aca aac gag ctg agt gat ttg gtt act tcc act ttg aac   1200
Gly Glu Gln Thr Asn Glu Leu Ser Asp Leu Val Thr Ser Thr Leu Asn
385                 390                 395                 400

tcc tcc att cca ttt gag ctt tct taa                              1227
Ser Ser Ile Pro Phe Glu Leu Ser
                405
```

<210> 30
<211> 408
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 30

```
Met Ala Pro Pro Arg Leu Cys Ile Arg Val Asn Asn Ser Glu Leu Phe
 1               5                  10                  15
Phe Val Ala Ser Glu Ser Ser Tyr Asn Glu Asn Asp Ile Asn Thr Pro
            20                  25                  30
Lys Glu Ile Asp Asp Thr Thr Asn Leu Asn Asn Asn Tyr Arg Asn Asn
        35                  40                  45
Leu Asp Glu Val Ile Leu Asp Tyr Asn Ser Gln Thr Ile Pro Gln Ile
    50                  55                  60
Ser Asn Arg Thr Leu Asn Thr Leu Val Gln Asp Asn Ser Tyr Val Pro
65                  70                  75                  80
Arg Tyr Asp Ser Asn Gly Thr Ser Glu Ile Glu Glu Tyr Asp Val Val
                85                  90                  95
Asp Phe Asn Val Phe Phe Tyr Leu His Ala Gln Lys Val Pro Glu Gly
            100                 105                 110
Glu Thr Asn Ile Ser Leu Thr Ser Ser Ile Asp Thr Ala Leu Leu Glu
        115                 120                 125
Glu Ser Lys Asp Ile Phe Phe Ser Ser Glu Phe Ile Asp Thr Ile Asn
    130                 135                 140
Lys Pro Val Asn Ala Ala Leu Phe Ile Asp Trp Ile Ser Lys Val Ile
145                 150                 155                 160
Arg Asp Phe Thr Thr Glu Ala Thr Gln Lys Ser Thr Val Asp Lys Ile
                165                 170                 175
Ala Asp Ile Ser Leu Ile Val Pro Tyr Val Gly Leu Ala Leu Asn Ile
            180                 185                 190
Ile Ile Glu Ala Glu Lys Gly Asn Phe Glu Glu Ala Phe Glu Leu Leu
        195                 200                 205
Gly Val Gly Ile Leu Leu Glu Phe Val Pro Glu Leu Thr Ile Pro Val
    210                 215                 220
Ile Leu Val Phe Thr Ile Lys Ser Tyr Ile Asp Ser Tyr Glu Asn Lys
225                 230                 235                 240
Asn Lys Ala Ile Lys Ala Ile Asn Asn Ser Leu Ile Glu Arg Glu Ala
```

```
                245                 250                 255
Lys Trp Lys Glu Ile Tyr Ser Trp Ile Val Ser Asn Trp Leu Thr Arg
            260                 265                 270
Ile Asn Thr Gln Phe Asn Lys Arg Lys Glu Gln Met Tyr Gln Ala Leu
        275                 280                 285
Gln Asn Gln Val Asp Ala Ile Lys Thr Ala Ile Glu Tyr Lys Tyr Asn
    290                 295                 300
Asn Tyr Thr Ser Asp Glu Lys Asn Arg Leu Glu Ser Glu Tyr Asn Ile
305                 310                 315                 320
Asn Asn Ile Glu Glu Glu Leu Asn Lys Lys Val Ser Leu Ala Met Lys
                325                 330                 335
Asn Ile Glu Arg Phe Met Thr Glu Ser Ser Ile Ser Tyr Leu Met Lys
            340                 345                 350
Leu Ile Asn Glu Ala Lys Val Gly Lys Leu Lys Lys Tyr Asp Asn His
        355                 360                 365
Val Lys Ser Asp Leu Leu Asn Tyr Ile Leu Asp His Arg Ser Ile Leu
    370                 375                 380
Gly Glu Gln Thr Asn Glu Leu Ser Asp Leu Val Thr Ser Thr Leu Asn
385                 390                 395                 400
Ser Ser Ile Pro Phe Glu Leu Ser
                405
```

<210> 31
<211> 1233
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<221> CDS
<222> (1)...(1230)

<400> 31

```
atg gcc aaa aat acc ggt aaa tct gaa cag tgt att att gtt aat aat   48
Met Ala Lys Asn Thr Gly Lys Ser Glu Gln Cys Ile Ile Val Asn Asn
 1               5                  10                  15

gag gat tta ttt ttc ata gct aat aaa gat agt ttt tca aaa gat tta   96
Glu Asp Leu Phe Phe Ile Ala Asn Lys Asp Ser Phe Ser Lys Asp Leu
             20                  25                  30

gct aaa gca gaa act ata gca tat aat aca caa aat aat act ata gaa   144
Ala Lys Ala Glu Thr Ile Ala Tyr Asn Thr Gln Asn Asn Thr Ile Glu
         35                  40                  45

aat aat ttt tct ata gat cag ttg att tta gat aat gat tta agc agt   192
Asn Asn Phe Ser Ile Asp Gln Leu Ile Leu Asp Asn Asp Leu Ser Ser
     50                  55                  60

ggc ata gac tta cca aat gaa aac aca gaa cca ttt aca aat ttt gac   240
Gly Ile Asp Leu Pro Asn Glu Asn Thr Glu Pro Phe Thr Asn Phe Asp
 65                  70                  75                  80

gac ata gat atc cct gtg tat att aaa caa tct gct tta aaa aaa att   288
Asp Ile Asp Ile Pro Val Tyr Ile Lys Gln Ser Ala Leu Lys Lys Ile
```

```
                85                  90                  95

ttt gtg gat gga gat agc ctt ttt gaa tat tta cat gct caa aca ttt   336
Phe Val Asp Gly Asp Ser Leu Phe Glu Tyr Leu His Ala Gln Thr Phe
            100                 105                 110

cct tct aat ata gaa aat cta caa cta acg aat tca tta aat gat gct   384
Pro Ser Asn Ile Glu Asn Leu Gln Leu Thr Asn Ser Leu Asn Asp Ala
        115                 120                 125

tta aga aat aat aat aaa gtc tat act ttt ttt tct aca aac ctt gtt   432
Leu Arg Asn Asn Asn Lys Val Tyr Thr Phe Phe Ser Thr Asn Leu Val
    130                 135                 140

gaa aaa gct aat aca gtt gta ggt gct tca ctt ttt gta aac tgg gta   480
Glu Lys Ala Asn Thr Val Val Gly Ala Ser Leu Phe Val Asn Trp Val
145                 150                 155                 160

aaa gga gta ata gat gat ttt aca tct gaa tcc aca caa aaa agt act   528
Lys Gly Val Ile Asp Asp Phe Thr Ser Glu Ser Thr Gln Lys Ser Thr
                165                 170                 175

ata gat aaa gtt tca gat gta tcc ata att att ccc tat ata gga cct   576
Ile Asp Lys Val Ser Asp Val Ser Ile Ile Ile Pro Tyr Ile Gly Pro
            180                 185                 190

gct ttg aat gta gga aat gaa aca gct aaa gaa aat ttt aaa aat gct   624
Ala Leu Asn Val Gly Asn Glu Thr Ala Lys Glu Asn Phe Lys Asn Ala
        195                 200                 205

ttt gaa ata ggt gga gcc gct atc tta atg gag ttt att cca gaa ctt   672
Phe Glu Ile Gly Gly Ala Ala Ile Leu Met Glu Phe Ile Pro Glu Leu
    210                 215                 220

att gta cct ata gtt gga ttt ttt aca tta gaa tca tat gta gga aat   720
Ile Val Pro Ile Val Gly Phe Phe Thr Leu Glu Ser Tyr Val Gly Asn
225                 230                 235                 240

aaa ggg cat att att atg acg ata tcc aat gct tta aag aaa agg gat   768
Lys Gly His Ile Ile Met Thr Ile Ser Asn Ala Leu Lys Lys Arg Asp
                245                 250                 255

caa aaa tgg aca gat atg tat ggt ttg ata gta tcg cag tgg ctc tca   816
Gln Lys Trp Thr Asp Met Tyr Gly Leu Ile Val Ser Gln Trp Leu Ser
            260                 265                 270

acg gtt aat act caa ttt tat aca ata aaa gaa aga atg tac aat gct   864
Thr Val Asn Thr Gln Phe Tyr Thr Ile Lys Glu Arg Met Tyr Asn Ala
        275                 280                 285

tta aat aat caa tca caa gca ata gaa aaa ata ata gaa gat caa tat   912
Leu Asn Asn Gln Ser Gln Ala Ile Glu Lys Ile Ile Glu Asp Gln Tyr
    290                 295                 300

aat aga tat agt gaa gaa gat aaa atg aat att aac att gat ttt aat   960
Asn Arg Tyr Ser Glu Glu Asp Lys Met Asn Ile Asn Ile Asp Phe Asn
305                 310                 315                 320
```

```
gat ata gat ttt aaa ctt aat caa agt ata aat tta gca ata aac aat   1008
Asp Ile Asp Phe Lys Leu Asn Gln Ser Ile Asn Leu Ala Ile Asn Asn
                325                 330                 335

ata gat gat ttt ata aac caa tgt tct ata tca tat cta atg aat aga   1056
Ile Asp Asp Phe Ile Asn Gln Cys Ser Ile Ser Tyr Leu Met Asn Arg
            340                 345                 350

atg att cca tta gct gta aaa aag tta aaa gac ttt gat gat aat ctt   1104
Met Ile Pro Leu Ala Val Lys Lys Leu Lys Asp Phe Asp Asp Asn Leu
        355                 360                 365

aag aga gat tta ttg gag tat ata gat aca aat gaa cta tat tta ctt   1152
Lys Arg Asp Leu Leu Glu Tyr Ile Asp Thr Asn Glu Leu Tyr Leu Leu
    370                 375                 380

gat gaa gta aat att cta aaa tca aaa gta aat aga cac cta aaa gac   1200
Asp Glu Val Asn Ile Leu Lys Ser Lys Val Asn Arg His Leu Lys Asp
385                 390                 395                 400

agt ata cca ttt gat ctt tca cta tat acc taa                      1233
Ser Ile Pro Phe Asp Leu Ser Leu Tyr Thr
                405                 410
```

<210> 32
<211> 410
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 32

```
Met Ala Lys Asn Thr Gly Lys Ser Glu Gln Cys Ile Ile Val Asn Asn
 1               5                  10                  15
Glu Asp Leu Phe Phe Ile Ala Asn Lys Asp Ser Phe Ser Lys Asp Leu
            20                  25                  30
Ala Lys Ala Glu Thr Ile Ala Tyr Asn Thr Gln Asn Asn Thr Ile Glu
        35                  40                  45
Asn Asn Phe Ser Ile Asp Gln Leu Ile Leu Asp Asn Asp Leu Ser Ser
    50                  55                  60
Gly Ile Asp Leu Pro Asn Glu Asn Thr Glu Pro Phe Thr Asn Phe Asp
65                  70                  75                  80
Asp Ile Asp Ile Pro Val Tyr Ile Lys Gln Ser Ala Leu Lys Lys Ile
                85                  90                  95
Phe Val Asp Gly Asp Ser Leu Phe Glu Tyr Leu His Ala Gln Thr Phe
            100                 105                 110
Pro Ser Asn Ile Glu Asn Leu Gln Leu Thr Asn Ser Leu Asn Asp Ala
        115                 120                 125
Leu Arg Asn Asn Asn Lys Val Tyr Thr Phe Phe Ser Thr Asn Leu Val
    130                 135                 140
Glu Lys Ala Asn Thr Val Val Gly Ala Ser Leu Phe Val Asn Trp Val
145                 150                 155                 160
Lys Gly Val Ile Asp Asp Phe Thr Ser Glu Ser Thr Gln Lys Ser Thr
                165                 170                 175
```

```
Ile Asp Lys Val Ser Asp Val Ser Ile Ile Ile Pro Tyr Ile Gly Pro
            180                 185                 190
Ala Leu Asn Val Gly Asn Glu Thr Ala Lys Glu Asn Phe Lys Asn Ala
        195                 200                 205
Phe Glu Ile Gly Gly Ala Ala Ile Leu Met Glu Phe Ile Pro Glu Leu
    210                 215                 220
Ile Val Pro Ile Val Gly Phe Phe Thr Leu Glu Ser Tyr Val Gly Asn
225                 230                 235                 240
Lys Gly His Ile Ile Met Thr Ile Ser Asn Ala Leu Lys Lys Arg Asp
                245                 250                 255
Gln Lys Trp Thr Asp Met Tyr Gly Leu Ile Val Ser Gln Trp Leu Ser
            260                 265                 270
Thr Val Asn Thr Gln Phe Tyr Thr Ile Lys Glu Arg Met Tyr Asn Ala
        275                 280                 285
Leu Asn Asn Gln Ser Gln Ala Ile Glu Lys Ile Ile Glu Asp Gln Tyr
    290                 295                 300
Asn Arg Tyr Ser Glu Glu Asp Lys Met Asn Ile Asn Ile Asp Phe Asn
305                 310                 315                 320
Asp Ile Asp Phe Lys Leu Asn Gln Ser Ile Asn Leu Ala Ile Asn Asn
                325                 330                 335
Ile Asp Asp Phe Ile Asn Gln Cys Ser Ile Ser Tyr Leu Met Asn Arg
            340                 345                 350
Met Ile Pro Leu Ala Val Lys Lys Leu Lys Asp Phe Asp Asp Asn Leu
        355                 360                 365
Lys Arg Asp Leu Leu Glu Tyr Ile Asp Thr Asn Glu Leu Tyr Leu Leu
    370                 375                 380
Asp Glu Val Asn Ile Leu Lys Ser Lys Val Asn Arg His Leu Lys Asp
385                 390                 395                 400
Ser Ile Pro Phe Asp Leu Ser Leu Tyr Thr
                405                 410
```

<210> 33
<211> 1314
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<221> CDS
<222> (10)...(1305)

<400> 33

```
gaattcacg atg tct tac act aac gac aaa atc ctg atc ctg tac ttc aac 51
          Met Ser Tyr Thr Asn Asp Lys Ile Leu Ile Leu Tyr Phe Asn
           1               5                   10

aaa ctg tac aaa aaa atc aaa gac aac tct atc ctg gac atg cgt tac   99
Lys Leu Tyr Lys Lys Ile Lys Asp Asn Ser Ile Leu Asp Met Arg Tyr
 15                  20                  25                  30

gaa aac aac aaa ttc atc gac atc tct ggc tat ggt tct aac atc tct   147
Glu Asn Asn Lys Phe Ile Asp Ile Ser Gly Tyr Gly Ser Asn Ile Ser
                 35                  40                  45

atc aac ggt gac gtc tac atc tac tct act aac cgc aac cag ttc ggt   195
```

```
Ile Asn Gly Asp Val Tyr Ile Tyr Ser Thr Asn Arg Asn Gln Phe Gly
             50                  55                  60

atc tac tct tct aaa ccg tct gaa gta aac atc gct cag aac aac gac   243
Ile Tyr Ser Ser Lys Pro Ser Glu Val Asn Ile Ala Gln Asn Asn Asp
         65                  70                  75

atc atc tac aac ggt cgt tac cag aac ttc tct atc tct ttc tgg gtt   291
Ile Ile Tyr Asn Gly Arg Tyr Gln Asn Phe Ser Ile Ser Phe Trp Val
     80                  85                  90

cgt atc ccg aaa tac ttc aac aaa gtt aac ctg aac aac gaa tac act   339
Arg Ile Pro Lys Tyr Phe Asn Lys Val Asn Leu Asn Asn Glu Tyr Thr
 95                 100                 105                 110

atc atc gac tgc atc cgt aac aac aac tct ggt tgg aaa atc tct ctg   387
Ile Ile Asp Cys Ile Arg Asn Asn Asn Ser Gly Trp Lys Ile Ser Leu
                115                 120                 125

aac tac aac aaa atc atc tgg act ctg cag gac act gct ggt aac aac   435
Asn Tyr Asn Lys Ile Ile Trp Thr Leu Gln Asp Thr Ala Gly Asn Asn
            130                 135                 140

cag aaa ctg gtt ttc aac tac act cag atg atc tct atc tct gac tac   483
Gln Lys Leu Val Phe Asn Tyr Thr Gln Met Ile Ser Ile Ser Asp Tyr
        145                 150                 155

att aat aaa tgg atc ttc gtt act atc act aac aac cgt ctg ggt aac   531
Ile Asn Lys Trp Ile Phe Val Thr Ile Thr Asn Asn Arg Leu Gly Asn
    160                 165                 170

tct cgt atc tac atc aac ggt aac ctg atc gat gaa aaa tct atc tct   579
Ser Arg Ile Tyr Ile Asn Gly Asn Leu Ile Asp Glu Lys Ser Ile Ser
175                 180                 185                 190

aac ctg ggt gac atc cac gtt tct gac aac atc ctg ttc aaa atc gtt   627
Asn Leu Gly Asp Ile His Val Ser Asp Asn Ile Leu Phe Lys Ile Val
                195                 200                 205

ggt tgc aac gac acg cgt tac gtt ggt atc cgt tac ttc aaa gtt ttc   675
Gly Cys Asn Asp Thr Arg Tyr Val Gly Ile Arg Tyr Phe Lys Val Phe
            210                 215                 220

gac act gaa ctg ggt aaa act gaa atc gaa act ctg tac tct gac gaa   723
Asp Thr Glu Leu Gly Lys Thr Glu Ile Glu Thr Leu Tyr Ser Asp Glu
        225                 230                 235

ccg gac ccg tct atc ctg aaa gac ttc tgg ggt aac tac ctg ctg tac   771
Pro Asp Pro Ser Ile Leu Lys Asp Phe Trp Gly Asn Tyr Leu Leu Tyr
    240                 245                 250

aac aaa cgt tac tac ctg ctg aac ctg ctc cgg act gac aaa tct atc   819
Asn Lys Arg Tyr Tyr Leu Leu Asn Leu Leu Arg Thr Asp Lys Ser Ile
255                 260                 265                 270

act cag aac tct aac ttc ctg aac atc aac cag cag cgt ggt gtt tat   867
Thr Gln Asn Ser Asn Phe Leu Asn Ile Asn Gln Gln Arg Gly Val Tyr
```

```
                275                 280                 285

cag aaa cct aat atc ttc tct aac act cgt ctg tac act ggt gtt gaa   915
Gln Lys Pro Asn Ile Phe Ser Asn Thr Arg Leu Tyr Thr Gly Val Glu
            290                 295                 300

gtt atc atc cgt aaa aac ggt tct act gac atc tct aac act gac aac   963
Val Ile Ile Arg Lys Asn Gly Ser Thr Asp Ile Ser Asn Thr Asp Asn
        305                 310                 315

ttc gta cgt aaa aac gac ctg gct tac atc aac gtt gtt gac cgt gac   1011
Phe Val Arg Lys Asn Asp Leu Ala Tyr Ile Asn Val Val Asp Arg Asp
    320                 325                 330

gtt gaa tac cgt ctg tac gct gac atc tct atc gct aaa ccg gaa aaa   1059
Val Glu Tyr Arg Leu Tyr Ala Asp Ile Ser Ile Ala Lys Pro Glu Lys
335                 340                 345                 350

atc atc aaa ctg atc cgt act tct aac tct aac aac tct ctg ggt cag   1107
Ile Ile Lys Leu Ile Arg Thr Ser Asn Ser Asn Asn Ser Leu Gly Gln
                355                 360                 365

atc atc gtt atg gac tcg atc ggt aac aac tgc act atg aac ttc cag   1155
Ile Ile Val Met Asp Ser Ile Gly Asn Asn Cys Thr Met Asn Phe Gln
            370                 375                 380

aac aac aac ggt ggt aac atc ggt ctg ctg ggt ttc cac tct aac aac   1203
Asn Asn Asn Gly Gly Asn Ile Gly Leu Leu Gly Phe His Ser Asn Asn
        385                 390                 395

ctg gtt gct tct tca tgg tac tac aac aac atc cgt aaa aac act tct   1251
Leu Val Ala Ser Ser Trp Tyr Tyr Asn Asn Ile Arg Lys Asn Thr Ser
    400                 405                 410

tct aac ggt tgc ttc tgg tct ttc atc tct aaa gaa cac ggt tgg cag   1299
Ser Asn Gly Cys Phe Trp Ser Phe Ile Ser Lys Glu His Gly Trp Gln
415                 420                 425                 430

gaa aac taagaattc                                               1314
Glu Asn
```

<210> 34
<211> 432
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 34

```
Met Ser Tyr Thr Asn Asp Lys Ile Leu Ile Leu Tyr Phe Asn Lys Leu
 1               5                  10                  15
Tyr Lys Lys Ile Lys Asp Asn Ser Ile Leu Asp Met Arg Tyr Glu Asn
            20                  25                  30
Asn Lys Phe Ile Asp Ile Ser Gly Tyr Gly Ser Asn Ile Ser Ile Asn
```

```
        35                  40                  45
Gly Asp Val Tyr Ile Tyr Ser Thr Asn Arg Asn Gln Phe Gly Ile Tyr
    50                  55                  60
Ser Ser Lys Pro Ser Glu Val Asn Ile Ala Gln Asn Asn Asp Ile Ile
65                  70                  75                  80
Tyr Asn Gly Arg Tyr Gln Asn Phe Ser Ile Ser Phe Trp Val Arg Ile
                85                  90                  95
Pro Lys Tyr Phe Asn Lys Val Asn Leu Asn Asn Glu Tyr Thr Ile Ile
            100                 105                 110
Asp Cys Ile Arg Asn Asn Asn Ser Gly Trp Lys Ile Ser Leu Asn Tyr
        115                 120                 125
Asn Lys Ile Ile Trp Thr Leu Gln Asp Thr Ala Gly Asn Asn Gln Lys
    130                 135                 140
Leu Val Phe Asn Tyr Thr Gln Met Ile Ser Ile Ser Asp Tyr Ile Asn
145                 150                 155                 160
Lys Trp Ile Phe Val Thr Ile Thr Asn Asn Arg Leu Gly Asn Ser Arg
                165                 170                 175
Ile Tyr Ile Asn Gly Asn Leu Ile Asp Glu Lys Ser Ile Ser Asn Leu
            180                 185                 190
Gly Asp Ile His Val Ser Asp Asn Ile Leu Phe Lys Ile Val Gly Cys
        195                 200                 205
Asn Asp Thr Arg Tyr Val Gly Ile Arg Tyr Phe Lys Val Phe Asp Thr
    210                 215                 220
Glu Leu Gly Lys Thr Glu Ile Glu Thr Leu Tyr Ser Asp Glu Pro Asp
225                 230                 235                 240
Pro Ser Ile Leu Lys Asp Phe Trp Gly Asn Tyr Leu Leu Tyr Asn Lys
                245                 250                 255
Arg Tyr Tyr Leu Leu Asn Leu Leu Arg Thr Asp Lys Ser Ile Thr Gln
            260                 265                 270
Asn Ser Asn Phe Leu Asn Ile Asn Gln Gln Arg Gly Val Tyr Gln Lys
        275                 280                 285
Pro Asn Ile Phe Ser Asn Thr Arg Leu Tyr Thr Gly Val Glu Val Ile
    290                 295                 300
Ile Arg Lys Asn Gly Ser Thr Asp Ile Ser Asn Thr Asp Asn Phe Val
305                 310                 315                 320
Arg Lys Asn Asp Leu Ala Tyr Ile Asn Val Val Asp Arg Asp Val Glu
                325                 330                 335
Tyr Arg Leu Tyr Ala Asp Ile Ser Ile Ala Lys Pro Glu Lys Ile Ile
            340                 345                 350
Lys Leu Ile Arg Thr Ser Asn Ser Asn Asn Ser Leu Gly Gln Ile Ile
        355                 360                 365
Val Met Asp Ser Ile Gly Asn Asn Cys Thr Met Asn Phe Gln Asn Asn
    370                 375                 380
Asn Gly Gly Asn Ile Gly Leu Leu Gly Phe His Ser Asn Asn Leu Val
385                 390                 395                 400
Ala Ser Ser Trp Tyr Tyr Asn Asn Ile Arg Lys Asn Thr Ser Ser Asn
                405                 410                 415
Gly Cys Phe Trp Ser Phe Ile Ser Lys Glu His Gly Trp Gln Glu Asn
            420                 425                 430
```